

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
16 September 2004 (16.09.2004)

PCT

(10) International Publication Number
WO 2004/079014 A2

- (51) International Patent Classification⁷: **C12Q 1/68**, (81) Designated States (*unless otherwise indicated, for every kind of national protection available*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.
- (21) International Application Number: PCT/US2004/006736
- (22) International Filing Date: 4 March 2004 (04.03.2004)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data: 60/451,942 4 March 2003 (04.03.2003) US
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- (84) Designated States (*unless otherwise indicated, for every kind of regional protection available*): ARIPO (BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).
- Published:**
— *without international search report and to be republished upon receipt of that report*
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

(54) Title: SIGNATURES OF ER STATUS IN BREAST CANCER

(57) Abstract: The invention relates to the identification and use of gene expression profiles, or patterns, suitable for identification of populations that are positive and negative for estrogen receptor expression. The gene expression profiles may be embodied in nucleic acid expression, protein expression, or other expression formats, and may be used in the study and/or diagnosis of cells and tissue in breast cancer as well as for the study and/or determination of prognosis of a patient, including breast cancer survival.



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Signatures of ER Status in Breast Cancer

RELATED APPLICATIONS

This application claims benefit of priority from U.S. Provisional Patent
5 application 60/451,942, filed March 4, 2003, which is hereby incorporated by
reference in its entirety as if fully set forth.

FIELD OF THE INVENTION

The invention relates to the identification and use of gene expression profiles,
10 or patterns, involved in breast cancer survival. In particular, the invention provides
the identities of genes that may be used to identify populations that are positive and
negative for estrogen receptor expression. The gene expression profiles, whether
embodied in nucleic acid expression, protein expression, or other expression formats,
are used in the study and/or diagnosis of cells and tissue in breast cancer as well as for
15 the study and/or determination of prognosis of a patient. The profiles may also be
used in methods of diagnosis or prognosis.

BACKGROUND OF THE INVENTION

Breast cancer is by far the most common cancer among women. Each year,
20 more than 180,000 and 1 million women in the U.S. and worldwide, respectively, are
diagnosed with breast cancer. Breast cancer is the leading cause of death for women
between ages 50-55, and is the most common non-preventable malignancy in women
in the Western Hemisphere. An estimated 2,167,000 women in the United States are
currently living with the disease (National Cancer Institute, Surveillance
25 Epidemiology and End Results (NCI SEER) program, *Cancer Statistics Review*
(CSR), www-seer.ims.nci.nih.gov/Publications/CSR1973 (1998)). Based on cancer
rates from 1995 through 1997, a report from the National Cancer Institute (NCI)
estimates that about 1 in 8 women in the United States (approximately 12.8 percent)
will develop breast cancer during her lifetime (NCI's Surveillance, Epidemiology, and
30 End Results Program (SEER) publication *SEER Cancer Statistics Review 1973-1997*).

Breast cancer is the second most common form of cancer, after skin cancer, among women in the United States. An estimated 250,100 new cases of breast cancer are expected to be diagnosed in the United States in 2001. Of these, 192,200 new cases of more advanced (invasive) breast cancer are expected to occur among women (an
5 increase of 5% over last year), 46,400 new cases of early stage (*in situ*) breast cancer are expected to occur among women (up 9% from last year), and about 1,500 new cases of breast cancer are expected to be diagnosed in men (Cancer Facts & Figures 2001 American Cancer Society). An estimated 40,600 deaths (40,300 women, 400 men) from breast cancer are expected in 2001. Breast cancer ranks second only to
10 lung cancer among causes of cancer deaths in women. Nearly 86% of women who are diagnosed with breast cancer are likely to still be alive five years later, though 24% of them will die of breast cancer after 10 years, and nearly half (47%) will die of breast cancer after 20 years.

Every woman is at risk for breast cancer. Over 70 percent of breast cancers
15 occur in women who have no identifiable risk factors other than age (U.S. General Accounting Office. Breast Cancer, 1971-1991: Prevention, Treatment and Research. GAO/PEMD-92-12; 1991). Only 5 to 10% of breast cancers are linked to a family history of breast cancer (Henderson IC, Breast Cancer. In: Murphy GP, Lawrence WL, Lenhard RE (eds). *Clinical Oncology*. Atlanta, GA: American Cancer Society;
20 1995:198-219).

Each breast has 15 to 20 sections called lobes. Within each lobe are many smaller lobules. Lobules end in dozens of tiny bulbs that can produce milk. The lobes, lobules, and bulbs are all linked by thin tubes called ducts. These ducts lead to the nipple in the center of a dark area of skin called the areola. Fat surrounds the
25 lobules and ducts. There are no muscles in the breast, but muscles lie under each breast and cover the ribs. Each breast also contains blood vessels and lymph vessels. The lymph vessels carry colorless fluid called lymph, and lead to the lymph nodes. Clusters of lymph nodes are found near the breast in the axilla (under the arm), above the collarbone, and in the chest.

30 Breast tumors can be either benign or malignant. Benign tumors are not cancerous, they do not spread to other parts of the body, and are not a threat to life.

They can usually be removed, and in most cases, do not come back. Malignant tumors are cancerous, and can invade and damage nearby tissues and organs. Malignant tumor cells may metastasize, entering the bloodstream or lymphatic system. When breast cancer cells metastasize outside the breast, they are often found
5 in the lymph nodes under the arm (axillary lymph nodes). If the cancer has reached these nodes, it means that cancer cells may have spread to other lymph nodes or other organs, such as bones, liver, or lungs.

Major and intensive research has been focussed on early detection, treatment and prevention. This has included an emphasis on determining the presence of
10 precancerous or cancerous ductal epithelial cells. These cells are analyzed, for example, for cell morphology, for protein markers, for nucleic acid markers, for chromosomal abnormalities, for biochemical markers, and for other characteristic changes that would signal the presence of cancerous or precancerous cells. This has led to various molecular alterations that have been reported in breast cancer, few of
15 which have been well characterized in human clinical breast specimens. Molecular alterations include presence/absence of estrogen and progesterone steroid receptors, HER-2 expression/amplification (Mark HF, et al. HER-2/neu gene amplification in stages I-IV breast cancer detected by fluorescent in situ hybridization. Genet Med; 1(3):98-103 1999), Ki-67 (an antigen that is present in all stages of the cell cycle
20 except G0 and used as a marker for tumor cell proliferation, and prognostic markers (including oncogenes, tumor suppressor genes, and angiogenesis markers) like p53, p27, Cathepsin D, pS2, multi-drug resistance (MDR) gene, and CD31.

Estrogen receptor (ER) status has been of particular interest because it has been correlated with prognosis and treatment regimens. Generally speaking, patients
25 identified as having ER positive breast cancer biopsies have a better overall survival expectation while patients with ER negative biopsies are treated more aggressively, such as with immediate chemotherapy after surgical intervention, because of a poor prognosis.

Citation of documents herein is not intended as an admission that any is
30 pertinent prior art. All statements as to the date or representation as to the contents of documents is based on the information available to the applicant and does not

constitute any admission as to the correctness of the dates or contents of the documents.

SUMMARY OF THE INVENTION

5 The present invention relates to the identification and use of gene expression patterns (or profiles or "signatures") which are correlated with (and thus able to discriminate between) cells that are positive or negative for estrogen receptor (ER) expression in breast cancer specimens. The patterns may thus serve as a supplement to assays for ER status in breast cancer samples or used as a substitute for known
10 assays for ER status. The patterns may thus be used in diagnostic or prognostic methods or assays in the clinic to determine the course of treatment following identification of the presence of breast cancer or subsequent surgical removal thereof.

 The patterns also provide the identity of genes that may be the focus of therapeutic efforts to identify agents and treatment methods to alleviate the severity of
15 breast cancer, improve the chances for surviving breast cancer, and/or decrease the chances of breast cancer recurrence or metastases. Such agents and methods may be used to increase or decrease the expression of one or more genes of the patterns to restore cells to a less cancerous state or a state with a better prognosis for the patient. The patterns may also be used to identify cellular mechanisms or pathways, as well as
20 the components of such mechanisms or pathways, to be altered or modulated in the treatment of breast cancer.

 The present invention provides a non-subjective means for the identification of ER status in breast cancer samples by assaying for the expression patterns associated with ER status. Thus subjective interpretation is necessary and a more accurate
25 assessment of ER status, and breast cancer status and prognosis, is provided. Furthermore, the expression patterns can also be used as a means to assay small, node negative tumors that are not readily assayed by other means.

 The gene expression patterns comprise one or more than one gene capable of discriminating between breast cancer that is ER positive or ER negative with
30 significant accuracy. The gene(s) are identified as correlated with ER expression status in breast cancer such that the levels of their expression are relevant to a

determination of ER status in breast cancer of a cell. Thus in one aspect, the invention provides a method to determine the ER status of breast cancer of a subject afflicted with, or suspected of having, breast cancer by assaying a cell containing sample from said subject for expression of one or more than one gene disclosed herein
5 as correlated with ER status in breast cancer.

Gene expression patterns of the invention are identified by analysis of gene expression in multiple samples of ER positive and ER negative samples from breast cancer biopsies. The overall gene expression profile of a sample is obtained through quantifying the expression levels of mRNA corresponding to multiple genes to
10 identify genes that are positively, or negatively, correlated, with ER positive and ER negative sample.

A profile of genes that are highly correlated with ER status may be used to assay an sample from a subject afflicted with, or suspected of having, breast cancer to identify the ER status of breast cancer to which the sample belongs. This may be
15 done in combination with, or separate from a direct assay for ER expression. Such assays may be used as part of a method to determine the therapeutic treatment for said subject based upon the ER status identified. The present invention also provides for the advantageous ability to determine ER status in combination with other information to provide more detailed information in diagnosing and treating breast
20 cancer.

The correlated genes may be used singly with significant accuracy or in combination to increase the ability to accurately identify ER status. The present invention thus provides means for correlating a molecular expression phenotype with ER expression and thus a physiological (cellular) state. This correlation also provides
25 a way to molecularly diagnose and/or monitor a cell's status. Additional uses of the correlated gene(s) are in the classification of cells and tissues; determination of diagnosis and/or prognosis; and determination and/or alteration of therapy.

An assay of the invention may utilize a means related to the expression level of the sequences disclosed herein as long as the assay reflects, quantitatively or
30 qualitatively, expression of the sequence. Preferably, however, a quantitative assay means is preferred. The ability to discriminate is conferred by the identification of

expression of the individual genes as relevant and not by the form of the assay used to determine the actual level of expression. An assay may utilize any identifying feature of an identified individual gene as disclosed herein as long as the assay reflects, quantitatively or qualitatively, expression of the gene. Identifying features include, but are not limited to, unique nucleic acid sequences used to encode (DNA), or
5 express (RNA), said gene or epitopes specific to, or activities of, a protein encoded by said gene. Alternative means include detection of nucleic acid amplification as indicative of increased expression levels and nucleic acid inactivation, deletion, or methylation, as indicative of decreased expression levels. Stated differently, the
10 invention may be practiced by assaying one or more aspect of the DNA template(s) underlying the expression of the disclosed sequence(s), of the RNA used as an intermediate to express the sequence(s), or of the proteinaceous product expressed by the sequence(s), as well as proteolytic fragments of such products. As such, the detection of the presence of, amount of, stability of, or degradation (including rate) of,
15 such DNA, RNA and proteinaceous molecules may be used in the practice of the invention. As such, all that is required is the identity of the gene(s) necessary to discriminate between ER positive and negative samples and an appropriate cell containing sample for use in an expression assay.

In one aspect, the invention provides for the identification of the gene
20 expression patterns by analyzing global, or near global, gene expression from single cells or homogenous cell populations which have been dissected away from, or otherwise isolated or purified from, contaminating cells beyond that possible by a simple biopsy. Because the expression of numerous genes fluctuate between cells from different patients as well as between cells from the same patient sample, the
25 expression of multiple individual genes may be analyzed to for the best the ability to discriminate ER positive and negative samples.

In a further aspect, the gene(s) capable of discriminating between ER positive and negative samples may be used to identify ER status of an unknown sample of cell(s) from the breast. Preferably, the sample is isolated via non-invasive means.
30 The expression of said gene(s) in said unknown sample may be determined and compared to the expression of said gene(s) in reference data of gene expression

patterns from ER positive and/or negative samples. Alternatively, the expression level may be compared to expression levels in normal or non-cancerous cells, preferably from the same sample or subject. In embodiments of the invention utilizing quantitative PCR, the expression level may be compared to expression levels
5 of reference genes in the same sample or a ratio of expression levels may be used. The invention provides for ratios of the expression level of a sequence that is underexpressed to the expression level of a sequence that is overexpressed as an indicator of ER positive or ER negative status. The use of a ratio can reduce comparisons with normal or non-cancerous cells.

10 One advantage provided by the present invention is that contaminating, non-breast cells (such as infiltrating lymphocytes or other immune system cells) are not present to possibly affect the genes identified or the subsequent analysis of gene expression to identify the status of suspected breast cancer cells. Such contamination is present where a biopsy is used to generate gene expression profiles.

15 While the present invention has been described mainly in the context of human breast cancer, it may be practiced in the context of breast cancer of any animal known to be potentially afflicted by breast cancer. Preferred animals for the application of the present invention are mammals, particularly those important to agricultural applications (such as, but not limited to, cattle, sheep, horses, and other
20 "farm animals") and for human companionship (such as, but not limited to, dogs and cats).

DETAILED DESCRIPTION OF THE SPECIFIC EMBODIMENTS

25 Definitions of terms as used herein:

A gene expression "pattern" or "profile" or "signature" refers to the relative expression of a gene between ER positive and negative cells which expression is correlated with being able to distinguish between ER positive and negative cells.

A "gene" is a polynucleotide that encodes a discrete product, whether RNA or
30 proteinaceous in nature. It is appreciated that more than one polynucleotide may be capable of encoding a discrete product. The term includes alleles and polymorphisms

of a gene that encodes the same product, or a functionally associated (including gain, loss, or modulation of function) analog thereof, based upon chromosomal location and ability to recombine during normal mitosis.

A "sequence" or "gene sequence" as used herein is a nucleic acid molecule or polynucleotide composed of a discrete order of nucleotide bases. The term includes the ordering of bases that encodes a discrete product (i.e. "coding region"), whether RNA or proteinaceous in nature, as well as the ordered bases that precede or follow a "coding region". Non-limiting examples of the latter include 5' and 3' untranslated regions of a gene. It is appreciated that more than one polynucleotide may be capable of encoding a discrete product. It is also appreciated that alleles and polymorphisms of the disclosed sequences may exist and may be used in the practice of the invention to identify the expression level(s) of the disclosed sequences or the allele or polymorphism. Identification of an allele or polymorphism depends in part upon chromosomal location and ability to recombine during mitosis.

The terms "correlate" or "correlation" or equivalents thereof refer to an association between expression of one or more genes and the ER status of a breast cancer cell and/or a breast cancer patient. A gene may be expressed at higher or lower levels and still be correlated with ER status and thus breast cancer survival or outcome. The invention provides for the correlation between increases, as well as decreases, in expression of gene sequences and ER positive or negative status. Increases and decreases may be readily expressed in the form of a ratio between expression in a non-normal cell and a normal cell such that a ratio of one (1) indicates no difference while ratios of two (2) and one-half indicate twice as much, and half as much, expression in the non-normal cell versus the normal cell, respectively. Expression levels can be readily determined by quantitative methods as described below.

For example, increases in gene expression can be indicated by ratios of or about 1.1, of or about 1.2, of or about 1.3, of or about 1.4, of or about 1.5, of or about 1.6, of or about 1.7, of or about 1.8, of or about 1.9, of or about 2, of or about 2.5, of or about 3, of or about 3.5, of or about 4, of or about 4.5, of or about 5, of or about 5.5, of or about 6, of or about 6.5, of or about 7, of or about 7.5, of or about 8, of or

about 8.5, of or about 9, of or about 9.5, of or about 10, of or about 15, of or about 20, of or about 30, of or about 40, of or about 50, of or about 60, of or about 70, of or about 80, of or about 90, of or about 100, of or about 150, of or about 200, of or about 300, of or about 400, of or about 500, of or about 600, of or about 700, of or about 800, of or about 900, or of or about 1000. A ratio of 2 is a 100% (or a two-fold) increase in expression. Decreases in gene expression can be indicated by ratios of or about 0.9, of or about 0.8, of or about 0.7, of or about 0.6, of or about 0.5, of or about 0.4, of or about 0.3, of or about 0.2, of or about 0.1, of or about 0.05, of or about 0.01, of or about 0.005, of or about 0.001, of or about 0.0005, of or about 0.0001, of or about 0.00005, of or about 0.00001, of or about 0.000005, or of or about 0.000001.

For a given phenotype, a ratio of the expression of a gene sequence expressed at increased levels in correlation with an ER status to the expression of a gene sequence expressed at decreased levels in correlation with the ER status may also be used as an indicator of the phenotype. As a non-limiting example, the ER positive status may be correlated with increased expression of a gene sequence overexpressed in ER positive cells as well as decreased expression of a gene sequence underexpressed in ER positive cells. Therefore, a ratio of the expression levels of the underexpressed sequence to the expression levels of the overexpressed sequence may be used as an indicator of ER status. Ratios comprising gene sequences that are differentially expressed in ER negative cells may also be used.

A "polynucleotide" is a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. This term refers only to the primary structure of the molecule. Thus, this term includes double- and single-stranded DNA and RNA. It also includes known types of modifications including labels known in the art, methylation, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, and internucleotide modifications such as uncharged linkages (e.g., phosphorothioates, phosphorodithioates, etc.), as well as unmodified forms of the polynucleotide.

The term "amplify" is used in the broad sense to mean creating an amplification product can be made enzymatically with DNA or RNA polymerases. "Amplification," as used herein, generally refers to the process of producing multiple

copies of a desired sequence, particularly those of a sample. "Multiple copies" mean at least 2 copies. A "copy" does not necessarily mean perfect sequence complementarity or identity to the template sequence.

By corresponding is meant that a nucleic acid molecule shares a substantial
5 amount of sequence identity with another nucleic acid molecule. Substantial amount means at least 95%, usually at least 98% and more usually at least 99%, and sequence identity is determined using the BLAST algorithm, as described in Altschul et al. (1990), J. Mol. Biol. 215:403-410 (using the published default setting, i.e. parameters $w=4$, $t=17$). Methods for amplifying mRNA are generally known in the art, and
10 include reverse transcription PCR (RT-PCR) and those described in U.S. Patent Application 10/062,857 (filed on October 25, 2001), as well as U.S. Provisional Patent Applications 60/298,847 (filed June 15, 2001) and 60/257,801 (filed December 22, 2000), all of which are hereby incorporated by reference in their entireties as if fully set forth. Another method which may be used is quantitative PCR (or Q-PCR).
15 Alternatively, RNA may be directly labeled as the corresponding cDNA by methods known in the art.

A "microarray" is a linear or two-dimensional array of preferably discrete regions, each having a defined area, formed on the surface of a solid support such as, but not limited to, glass, plastic, or synthetic membrane. The density of the discrete
20 regions on a microarray is determined by the total numbers of immobilized polynucleotides to be detected on the surface of a single solid phase support, preferably at least about $50/\text{cm}^2$, more preferably at least about $100/\text{cm}^2$, even more preferably at least about $500/\text{cm}^2$, but preferably below about $1,000/\text{cm}^2$. Preferably, the arrays contain less than about 500, about 1000, about 1500, about 2000, about
25 2500, or about 3000 immobilized polynucleotides in total. As used herein, a DNA microarray is an array of oligonucleotides or polynucleotides placed on a chip or other surfaces used to hybridize to amplified or cloned polynucleotides from a sample. Since the position of each particular group of primers in the array is known, the identities of a sample polynucleotides can be determined based on their binding to a
30 particular position in the microarray.

Because the invention relies upon the identification of genes that are over- or under-expressed, one embodiment of the invention involves determining expression by hybridization of mRNA, or an amplified or cloned version thereof, of a sample cell to a polynucleotide that is unique to a particular gene sequence. Preferred
5 polynucleotides of this type contain at least about 20, at least about 22, at least about 24, at least about 26, at least about 28, at least about 30, or at least about 32 consecutive basepairs of a gene sequence that is not found in other gene sequences. The term "about" as used in the previous sentence refers to an increase or decrease of 1 from the stated numerical value. Even more preferred are polynucleotides of at
10 least or about 50, at least or about 100, at least about or 150, at least or about 200, at least or about 250, at least or about 300, at least or about 350, or at least or about 400 basepairs of a gene sequence that is not found in other gene sequences. The term "about" as used in the preceding sentence refers to an increase or decrease of 10% from the stated numerical value. Such polynucleotides may also be referred to as
15 polynucleotide probes that are capable of hybridizing to sequences of the genes, or unique portions thereof, described herein. Preferably, the sequences are those of mRNA encoded by the genes, the corresponding cDNA to such mRNAs, and/or amplified versions of such sequences. In preferred embodiments of the invention, the polynucleotide probes are immobilized on an array, other devices, or in individual
20 spots that localize the probes.

In another embodiment of the invention, all or part of a disclosed sequence may be amplified and detected by methods such as the polymerase chain reaction (PCR) and variations thereof, such as, but not limited to, quantitative PCR (Q-PCR), reverse transcription PCR (RT-PCR), and real-time PCR (including as a means of
25 measuring the initial amounts of mRNA copies for each sequence in a sample), optionally real-time RT-PCR or real-time Q-PCR. Such methods would utilize one or two primers that are complementary to portions of a disclosed sequence, where the primers are used to prime nucleic acid synthesis. The newly synthesized nucleic acids are optionally labeled and may be detected directly or by hybridization to a
30 polynucleotide of the invention. The newly synthesized nucleic acids may be contacted with polynucleotides (containing sequences) of the invention under

conditions which allow for their hybridization. Additional methods to detect the expression of expressed nucleic acids include RNase protection assays, including liquid phase hybridizations, and *in situ* hybridization of cells.

Alternatively, and in yet another embodiment of the invention, gene
5 expression may be determined by analysis of expressed protein in a cell sample of interest by use of one or more antibodies specific for one or more epitopes of individual gene products (proteins), or proteolytic fragments thereof, in said cell sample or in a bodily fluid of a subject. The cell sample may be one of breast cancer epithelial cells enriched from the blood of a subject, such as by use of labeled
10 antibodies against cell surface markers followed by fluorescence activated cell sorting (FACS). Such antibodies are preferably labeled to permit their easy detection after binding to the gene product. Detection methodologies suitable for use in the practice of the invention include, but are not limited to, immunohistochemistry of cell containing samples or tissue, enzyme linked immunosorbent assays (ELISAs)
15 including antibody sandwich assays of cell containing tissues or blood samples, mass spectroscopy, and immuno-PCR.

The term "label" refers to a composition capable of producing a detectable signal indicative of the presence of the labeled molecule. Suitable labels include radioisotopes, nucleotide chromophores, enzymes, substrates, fluorescent molecules,
20 chemiluminescent moieties, magnetic particles, bioluminescent moieties, and the like. As such, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means.

The term "support" refers to conventional supports such as beads, particles, dipsticks, fibers, filters, membranes and silane or silicate supports such as glass slides.

25 As used herein, a "breast tissue sample" or "breast cell sample" refers to a sample of breast tissue or fluid isolated from an individual suspected of being afflicted with, or at risk of developing, breast cancer. Such samples are primary isolates (in contrast to cultured cells) and may be collected by any non-invasive means, including, but not limited to, ductal lavage, fine needle aspiration, needle
30 biopsy, the devices and methods described in U.S. Patent 6,328,709, or any other suitable means recognized in the art. Alternatively, the "sample" may be collected by

an invasive method, including, but not limited to, surgical biopsy. A sample of the invention may also be one that has been formalin fixed and paraffin embedded (FFPE).

5 “Expression” and “gene expression” include transcription and/or translation of nucleic acid material.

As used herein, the term “comprising” and its cognates are used in their inclusive sense; that is, equivalent to the term “including” and its corresponding cognates.

10 Conditions that “allow” an event to occur or conditions that are “suitable” for an event to occur, such as hybridization, strand extension, and the like, or “suitable” conditions are conditions that do not prevent such events from occurring. Thus, these conditions permit, enhance, facilitate, and/or are conducive to the event. Such conditions, known in the art and described herein, depend upon, for example, the nature of the nucleotide sequence, temperature, and buffer conditions. These
15 conditions also depend on what event is desired, such as hybridization, cleavage, strand extension or transcription.

Sequence “mutation,” as used herein, refers to any sequence alteration in the sequence of a gene disclosed herein interest in comparison to a reference sequence. A sequence mutation includes single nucleotide changes, or alterations of more than one
20 nucleotide in a sequence, due to mechanisms such as substitution, deletion or insertion. Single nucleotide polymorphism (SNP) is also a sequence mutation as used herein. Because the present invention is based on the relative level of gene expression, mutations in non-coding regions of genes as disclosed herein may also be assayed in the practice of the invention.

25 “Detection” includes any means of detecting, including direct and indirect detection of gene expression and changes therein. For example, “detectably less” products may be observed directly or indirectly, and the term indicates any reduction (including the absence of detectable signal). Similarly, “detectably more” product means any increase, whether observed directly or indirectly.

30 Increases and decreases in expression of the disclosed sequences are defined in the following terms based upon percent or fold changes over expression in normal

cells. Increases may be of 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, or 200% relative to expression levels in normal cells. Alternatively, fold increases may be of 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, or 10 fold over expression levels in normal cells. Decreases may be of 10, 20, 30, 40, 50, 55,
5 60, 65, 70, 75, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 99 or 100% relative to expression levels in normal cells.

Unless defined otherwise all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs.

10

Specific Embodiments

The present invention relates to the identification and use of gene expression patterns (or profiles or "signatures") which discriminate between (or are correlated with) breast cancer cells that are ER positive or negative, preferably ER α positive or
15 negative. Because the overall gene expression profile differs from person to person, cancer to cancer, and cancer cell to cancer cell, correlations between genes expressed or underexpressed in ER positive and negative cells are capable of identifying ER status. ER status has been used as a factor in determinations of therapeutic treatment of patients with breast cancer. For example, ER positive status has been used as an
20 indicator of responsiveness to treatment with tamoxifen and other selective estrogen receptor modulators (SERMs).

The present invention may be practiced with any subset of the genes disclosed herein. Gene expression in cells of breast cancer biopsies were used to identify thousands of genes capable of discriminating between ER positive and negative breast
25 cancer cells as described in the following Example. The identification may be made by using expression profiles of various homogenous breast cancer cell populations, which are optionally isolated by microdissection, such as, but not limited to, laser capture microdissection (LCM) of 100-1000 cells.

Genes that are identified as being expressed differently between ER positive
30 and ER negative cells may be analyzed by standard statistical analysis, such as the t-test, to assign a value for the significance of the difference. Genes with a significance

above a particular threshold may be included in a pattern that segregates breast cancer based on ER status.

The expression of other genes in a breast cancer cell would be relatively unable to provide information concerning, and thus assist in the discrimination of, ER status in breast cancer.

To determine the (increased or decreased) expression levels of genes in the practice of the present invention, any method known in the art may be utilized. In one preferred embodiment of the invention, expression based on detection of RNA which hybridizes to the genes identified and disclosed herein is used. This is readily performed by any RNA detection or amplification+detection method known or recognized as equivalent in the art such as, but not limited to, reverse transcription-PCR, the methods disclosed in U.S. Patent Application 10/062,857 (filed on October 25, 2001) as well as U.S. Provisional Patent Applications 60/298,847 (filed June 15, 2001) and 60/257,801 (filed December 22, 2000), and methods to detect the presence, or absence, of RNA stabilizing or destabilizing sequences.

Alternatively, expression based on detection of DNA status may be used. Detection of the DNA of an identified gene as methylated or deleted may be used for genes that have decreased expression in correlation with ER status. This may be readily performed by PCR based methods known in the art, including, but not limited to, quantitative PCR (Q-PCR). Conversely, detection of the DNA of an identified gene as amplified may be used for genes that have increased expression in correlation with ER status. This may be readily performed by PCR based, fluorescent *in situ* hybridization (FISH) and chromosome *in situ* hybridization (CISH) methods known in the art.

Expression based on detection of a presence, increase, or decrease in protein levels or activity may also be used. Detection may be performed by any immunohistochemistry (IHC) based, blood based (especially for secreted proteins), antibody (including autoantibodies against the protein) based, ex foliate cell (from the cancer) based, mass spectroscopy based, and image (including used of labeled ligand) based method known in the art and recognized as appropriate for the detection of the protein. Antibody and image based methods are additionally useful for the

localization of tumors after determination of cancer by use of cells obtained by a non-invasive procedure (such as ductal lavage or fine needle aspiration), where the source of the cancerous cells is not known. A labeled antibody or ligand may be used to localize the carcinoma(s) within a patient.

5 A preferred embodiment using a nucleic acid based assay to determine expression is by immobilization of one or more sequences of the genes identified herein on a solid support, including, but not limited to, a solid substrate as an array or to beads or bead based technology as known in the art. Alternatively, solution based expression assays known in the art may also be used. The immobilized gene(s) may
10 be in the form of polynucleotides that are unique or otherwise specific to the gene(s) such that the polynucleotide would be capable of hybridizing to a DNA or RNA corresponding to the gene(s). These polynucleotides may be the full length of the gene(s) or be short sequences of the genes (up to one nucleotide shorter than the full length sequence known in the art by deletion from the 5' or 3' end of the sequence)
15 that are optionally minimally interrupted (such as by mismatches or inserted non-complementary basepairs) such that hybridization with a DNA or RNA corresponding to the gene(s) is not affected. Preferably, the polynucleotides used are from the 3' end of the gene, such as within about 350, about 300, about 250, about 200, about 150, about 100, or about 50 nucleotides from the polyadenylation signal or polyadenylation
20 site of a gene or expressed sequence. Polynucleotides containing mutations relative to the sequences of the disclosed genes may also be used so long as the presence of the mutations still allows hybridization to produce a detectable signal.

 Alternatively, amplification of such sequences from the 3' end of genes by methods such as quantitative PCR may be used to determine the expression levels of
25 the sequences. The Ct values generated by such methods may be used to generate the ratios of expression levels as described herein.

 The immobilized gene(s) may be used to determine the state of nucleic acid samples prepared from sample breast cell(s) for which the ER status is not known or for confirmation of a status that is already assigned to the sample breast cell(s).
30 Without limiting the invention, such a cell may be from a patient suspected of being afflicted with, or at risk of developing, breast cancer. The immobilized

polynucleotide(s) need only be sufficient to specifically hybridize, optionally under stringent conditions, to the corresponding nucleic acid molecules derived from the sample. While even a single correlated gene sequence may be able to provide adequate accuracy in discriminating between ER status, two or more, three or more, 5 four or more, five or more, six or more, seven or more, eight or more, nine or more, ten or more, or eleven or more of the genes identified herein may be used as a subset capable of discriminating may be used in combination to increase the accuracy of the method. The invention specifically contemplates the selection of more than one, two or more, three or more, four or more, five or more, six or more, seven or more, eight 10 or more, nine or more, ten or more, or eleven or more of the genes disclosed in the tables and figures herein for use as a subset in the identification of whether a breast cancer sample is ER positive or negative.

Of course 15 or more, 20 or more, 30 or more, 40 or more, 50 or more, 60 or more, 70 or more, 80 or more, 90 or more, 100 or more, 150 or more, 200 or more, 15 250 or more, 300 or more, 350 or more, 400 or more, 450 or more, 500 or more, 600 or more, 700 or more, 800 or more, 900 or more, 1000 or more, or all the genes provided in Table 1 or 2 below may be used. Additionally, genes that identify ER positive and ER negative may be used together to permit differential identification of a test sample as being ER positive or ER negative.

20 In embodiments where only one or a few genes are to be analyzed, the nucleic acid derived from the sample breast cancer cell(s) may be preferentially amplified by use of appropriate primers such that only the genes to be analyzed are amplified to reduce contaminating background signals from other genes expressed in the breast cell. Alternatively, and where multiple genes are to be analyzed or where very few 25 cells (or one cell) is used, the nucleic acid from the sample may be globally amplified before hybridization to the immobilized polynucleotides. Of course RNA, or the cDNA counterpart thereof may be directly labeled and used, without amplification, by methods known in the art.

The invention is preferably practiced with unique sequences present within the 30 gene sequences disclosed herein. The uniqueness of a disclosed gene sequence refers to the portions or entireties of the sequences which are found in each gene to the

exclusion of other genes. Such unique sequences include those found at the 3' untranslated portion of the genes. Preferred unique sequences for the practice of the invention are those which contribute to the consensus sequences for each gene such that the unique sequences will be useful in detecting expression in a variety of individuals rather than being specific for a polymorphism present in some individuals. Alternatively, sequences unique to an individual or a subpopulation may be used. The preferred unique sequences are preferably of the lengths of polynucleotides of the invention as discussed herein.

In particularly preferred embodiments of the invention, polynucleotides having sequences present in the 3' untranslated and/or non-coding regions of the disclosed gene sequences are used to detect expression levels in breast cells. Such polynucleotides may optionally contain sequences found in the 3' portions of the coding regions of the disclosed sequences. Polynucleotides containing a combination of sequences from the coding and 3' non-coding regions preferably have the sequences arranged contiguously, with no intervening heterologous sequence(s).

Alternatively, the invention may be practiced with polynucleotides having sequences present in the 5' untranslated and/or non-coding regions of gene sequences in breast cells to detect their levels of expression. Such polynucleotides may optionally contain sequences found in the 5' portions of the coding regions. Polynucleotides containing a combination of sequences from the coding and 5' non-coding regions preferably have the sequences arranged contiguously, with no intervening heterologous sequence(s). The invention may also be practiced with sequences present in the coding regions of disclosed sequences.

Preferred polynucleotides contain sequences from 3' or 5' untranslated and/or non-coding regions of at least about 16, at least about 18, at least about 20, at least about 22, at least about 24, at least about 26, at least about 28, at least about 30, at least about 32, at least about 34, at least about 36, at least about 38, at least about 40, at least about 42, at least about 44, or at least about 46 consecutive nucleotides. The term "about" as used in the previous sentence refers to an increase or decrease of 1 from the stated numerical value. Even more preferred are polynucleotides containing sequences of at least or about 50, at least or about 100, at least about or 150, at least or

about 200, at least or about 250, at least or about 300, at least or about 350, or at least or about 400 consecutive nucleotides. The term "about" as used in the preceding sentence refers to an increase or decrease of 10% from the stated numerical value.

Sequences from the 3' or 5' end of the above described coding regions as
5 found in polynucleotides of the invention are of the same lengths as those described above, except that they would naturally be limited by the length of the coding region. The 3' end of a coding region may include sequences up to the 3' half of the coding region. Conversely, the 5' end of a coding region may include sequences up the 5' half of the coding region. Of course the above described sequences, or the coding
10 regions and polynucleotides containing portions thereof, may be used in their entirety.

Polynucleotides combining the sequences from a 3' untranslated and/or non-coding region and the associated 3' end of the coding region are preferably at least or about 100, at least about or 150, at least or about 200, at least or about 250, at least or
15 about 300, at least or about 350, or at least or about 400 consecutive nucleotides. Preferably, the polynucleotides used are from the 3' end of the gene, such as within about 350, about 300, about 250, about 200, about 150, about 100, or about 50 nucleotides from the polyadenylation signal or polyadenylation site of a gene or expressed sequence. Polynucleotides containing mutations relative to the sequences
20 of the disclosed genes may also be used so long as the presence of the mutations still allows hybridization to produce a detectable signal.

In another embodiment of the invention, polynucleotides containing deletions of nucleotides from the 5' and/or 3' end of the above disclosed sequences may be used. The deletions are preferably of 1-5, 5-10, 10-15, 15-20, 20-25, 25-30, 30-35,
25 35-40, 40-45, 45-50, 50-60, 60-70, 70-80, 80-90, 90-100, 100-125, 125-150, 150-175, or 175-200 nucleotides from the 5' and/or 3' end, although the extent of the deletions would naturally be limited by the length of the disclosed sequences and the need to be able to use the polynucleotides for the detection of expression levels.

Other polynucleotides of the invention from the 3' end of the above disclosed
30 sequences include those of primers and optional probes for quantitative PCR. Preferably, the primers and probes are those which amplify a region less than about

350, less than about 300, less than about 250, less than about 200, less than about 150, less than about 100, or less than about 50 nucleotides from the from the polyadenylation signal or polyadenylation site of a gene or expressed sequence.

In yet another embodiment of the invention, polynucleotides containing
5 portions of the above disclosed sequences including the 3' end may be used in the practice of the invention. Such polynucleotides would contain at least or about 50, at least or about 100, at least about or 150, at least or about 200, at least or about 250, at least or about 300, at least or about 350, or at least or about 400 consecutive nucleotides from the 3' end of the disclosed sequences.

10 The above assay embodiments may be used in a number of different ways to identify or detect ER status in a breast cancer cell sample from a patient. In many cases, this may reflect a secondary screen for the patient, who may have already undergone mammography or physical exam as a primary screen. If positive, the subsequent needle biopsy, ductal lavage, fine needle aspiration, or other analogous
15 methods may provide the sample for use in the above assay embodiments. The present invention is particularly useful in combination with non-invasive protocols, such as ductal lavage or fine needle aspiration, to prepare a breast cell sample.

The present invention provides an objective set of criteria, in the form of gene expression profiles of a discrete set of genes, to discriminate (or delineate) between
20 ER positive and negative breast cancer cells.

In one embodiment of the invention, the isolation and analysis of a breast cancer cell sample may be performed as follows:

- (1) Ductal lavage or other non-invasive procedure is performed on a patient to obtain a sample.
- 25 (2) Sample is prepared and coated onto a microscope slide. Note that ductal lavage results in clusters of cells that are cytologically examined as stated above.
- (3) Pathologist or image analysis software scans the sample for the presence of non-normal and/or atypical cells.
- 30 (4) If non-normal and/or atypical cells are observed, those cells are harvested (e.g. by microdissection such as LCM).

(5) RNA is extracted from the harvested cells.

(6) RNA is purified, amplified, and labeled.

(7) Labeled nucleic acid is contacted with a microarray containing

5 polynucleotides of the genes identified herein as correlated to discriminations between ER status under hybridization conditions to allow hybridization to occur, then processed and scanned to obtain a pattern of intensities of each spot (relative to a control for general gene expression in cells) which determine the level of expression of the gene(s) in the cells.

10 (8) The pattern of intensities is analyzed by comparison to the expression patterns of the genes in known samples of ER positive and negative breast cancer cells (relative to the same control).

A specific example of the above method would be performing ductal lavage following a primary screen, observing and collecting non-normal and/or atypical cells
15 for analysis. The comparison to known expression patterns, such as that made possible by a model based on the disclosed genes and patterns, identifies the cells as being ER positive or negative.

Alternatively, the sample may permit the collection of both normal as well as non-normal and/or atypical cells for analysis. The gene expression patterns for each
20 of these two samples will be compared to each other as well as the model and the normal versus individual abnormal comparisons therein based upon the reference data set. This approach can be significantly more powerful than the non-normal and/or atypical cells only approach because it utilizes significantly more information from the normal cells and the differences between normal and non-normal/atypical cells (in
25 both the sample and reference data sets) to determine the status of the non-normal and/or atypical cells from the sample.

With use of the present invention, skilled physicians may prescribe treatments based on non-invasive samples that they would have prescribed for a patient which had previously received a diagnosis via a solid tissue biopsy.

30 The above discussion is also applicable where a palpable lesion is detected followed by fine needle aspiration or needle biopsy of cells from the breast. The cells

are plated and reviewed by a pathologist or automated imaging system which selects cells for analysis as described above.

The present invention may also be used, however, with solid tissue biopsies. For example, a solid biopsy may be collected and prepared for visualization followed
5 by determination of expression of one or more genes identified herein to determine ER status in breast cancer. One preferred means is by use of *in situ* hybridization with polynucleotide or protein identifying probe(s) for assaying expression of said gene(s).

In an alternative method, the solid tissue biopsy may be used to extract
10 molecules followed by analysis for expression of one or more gene(s). This provides the ability to leave out the need for visualization and collection of only those cells suspected of being non-normal and/or atypical. This method may of course be modified such that only cells suspected of being non-normal and/or atypical are collected and used to extract molecules for analysis. This would require visualization
15 and selection as an prerequisite to gene expression analysis.

In a further modification of the above, both normal cells and cells suspected of being non-normal and/or atypical are collected and used to extract molecules for analysis of gene expression. The approach, benefits and results are as described above using non-invasive sampling.

20 The genes identified herein may be used to generate a model capable of predicting the breast cancer ER status of an unknown breast cell sample based on the expression of the identified genes in the sample.

The detection of gene expression from the samples may be by use of a single microarray able to assay gene expression of the genes disclosed herein, whether
25 correlated with ER positive or negative status.

Other uses of the present invention include providing the ability to identify breast cancer cell samples as being those of ER positive or negative for further research or study. This provides a particular advantage in many contexts requiring the identification of breast cancer ER status based on objective genetic or molecular
30 criteria.

The materials for use in the methods of the present invention are ideally suited for preparation of kits produced in accordance with well known procedures. The invention thus provides kits comprising agents for the detection of expression of the disclosed genes for identifying breast cancer ER status. Such kits optionally
5 comprising the agent with an identifying description or label or instructions relating to their use in the methods of the present invention, is provided. Such a kit may comprise containers, each with one or more of the various reagents (typically in concentrated form) utilized in the methods, including, for example, pre-fabricated microarrays, buffers, the appropriate nucleotide triphosphates (e.g., dATP, dCTP,
10 dGTP and dTTP; or rATP, rCTP, rGTP and UTP), reverse transcriptase, DNA polymerase, RNA polymerase, and one or more primer complexes of the present invention (e.g., appropriate length poly(T) or random primers linked to a promoter reactive with the RNA polymerase). A set of instructions will also typically be included.

15 The methods provided by the present invention may also be automated in whole or in part. All aspects of the present invention may also be practiced such that they consist essentially of a subset of the disclosed genes to the exclusion of material irrelevant to the identification of ER status.

The present invention also provides for the use of the gene product of one or
20 more of the disclosed gene in the identification of agents that increase or decrease the expression of, or the activity of, said gene product. Methods of identifying such agents are preferably used to identify agents that will return the expression of, or the activity of, a gene product to a more normal level as opposed to the level seen in ER positive or negative cell. Most preferred is the return of an ER negative cell to
25 normalcy in light of the poor prognosis for patients with ER negative status.

Such methods may be used to identify agents that decrease the expression of, or the activity of, a gene product encoded by a gene that is overexpressed in ER positive or ER negative cells. Alternatively, such methods may be used to identify agents that increase the expression of, or the activity of, a gene product encoded by a
30 gene that is underexpressed in ER positive or ER negative cells.

The following tables set forth the genes of the invention. For example, Tables 1 and 3 include the ESR1 (estrogen receptor alpha) gene. "CloneID" as used in the context of the present invention refers to the IMAGE Consortium clone ID number of each gene, the sequences of which are hereby incorporated by reference in their
5 entirety as they are available from the Consortium at image.llnl.gov as accessed on the filing date of the present application. "GeneID" as used in the context of the Tables herein as well as the present invention refers to the GenBank accession number of a sequence of each gene, the sequences of which are hereby incorporated by reference in their entirety as they are available from GenBank as accessed on the
10 filing date of the present application.

P value refers to values assigned as described in the Example below. The indications of "E-xx" where "xx" is a two digit number refers to alternative notation for exponential figures where "E-xx" is " 10^{-xx} ". Thus in combination with the numbers to the left of "E-xx", the value being represented is the numbers to the left
15 times 10^{-xx} . Chromosome Location refers to the human chromosome to which the gene has been assigned. Description provides a brief identifier of what the gene encodes/expresses.

Table 5 provides non-limiting examples of the corresponding GenBank accession number, clone ID number, and Unigene (cluster) ID numbers for exemplary
20 sequences disclosed herein. The sequences of the invention may thus be identified by any of these identifiers. The identification of other corresponding numbers (GenBank accession number, clone ID number, and/or Unigene (cluster) ID numbers) for sequences disclosed herein can be made as a matter of routine from public information sources and without undue experimentation.

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Table 1. Genes that are overexpressed in ER positive cells, and underexpressed in ER negative cells

Clone_ID	P_value	Gene_Description
2308409	0.001730688	KIAA1077 KIAA1077 protein
1569878	0.016682884	ESTs
757220	6.59E-06	FUS1 lung cancer candidate
1570414	0.001162673	DKFZP434J037 hypothetical protein DKFZp434J037
1459742	2.71E-09	MAP-1 modulator of apoptosis 1
455025	1.04E-05	CGR19 cell growth regulatory with ring finger domain
767784	0.001891407	JUND jun D proto-oncogene
1637767	1.80E-12	CS2 calsynenin-2
242778	2.42E-19	CEGP1 CEGP1 protein
897446	3.60E-05	ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]
50577	2.20E-05	MGC16028 MGC16028 similar to RIKEN cDNA 1700019E19 gene
566106	6.95E-05	Homo sapiens cDNA FLJ31200 fis, clone KIDNE2000574, weakly similar to Staphylococcus epidermidis putative cell-surface adhesin SdrF gene
785710	5.12E-05	KIAA1025 KIAA1025 protein
866702	0.034946932	PTPN13 protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)
431505	0.000107772	HS1-2 putative transmembrane protein
809876	7.98E-06	ATP5G2 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2
2321113	1.80E-12	AGR2 anterior gradient 2 (Xenopus laevis) homolog
1910426	0.016882187	BM-009 hypothetical protein
49249	0.000289664	Homo sapiens, clone MGC:10039 IMAGE:3889701, mRNA, complete cds
241043	0.009801049	Human clone 137308 mRNA, partial cds
111389	3.62E-12	ESTs
1866068	0.006067385	ESTs
590310	1.45E-10	Homo sapiens, clone MGC:17393 IMAGE:3914851, mRNA, complete cds
366966	0.004146925	Homo sapiens cDNA: FLJ21333 fis, clone COL02535
840506	0.021449552	3-Apr apoptosis related protein APR-3
1620396	0.04743837	ESTs

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307740	0.001654163 ESTs
1492780	0.040280641 ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
845453	0.016037507 ARL3 ADP-ribosylation factor-like 3
682817	0.01385764 MDM2 mouse double minute 2, human homolog of; p53-binding protein
773286	1.40E-08 SLC9A3R1 solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1
144029	0.007899024 EST
197775	3.62E-05 ESTs
796152	0.014513254 Homo sapiens cDNA FLJ11685 fis, clone HEMBA1004934
809892	1.77E-12 SEMA3B sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B
740941	4.14E-08 APM2 adipose specific 2
84965	0.000389422 C5orf3 chromosome 5 open reading frame 3
785732	2.50E-05 BM036 uncharacterized bone marrow protein BM036
417884	0.007045683 Homo sapiens cDNA FLJ12052 fis, clone HEMBB1002042, moderately similar to CYTOCHROME P450 4C1 (EC 1.14.14.1)
67988	5.65E-05 SNRPD2 small nuclear ribonucleoprotein D2 polypeptide (16.5kD)
342378	9.49E-06 DUSP5 dual specificity phosphatase 5
138550	0.006400652 FLJ11137 hypothetical protein FLJ11137
162753	0.043575209 DD5 progesterin induced protein
1881469	9.79E-05 OCLN occludin
136954	1.57E-07 ESTs, Weakly similar to YEX0_YEAST HYPOTHETICAL 64.8 KDA PROTEIN IN GDI1-COX15 INTERGENIC REGION [S.cerevisiae]
320456	0.00177597 FLJ10300 hypothetical protein FLJ10300
134270	0.02511167 Human hbc647 mRNA sequence
840524	0.011860244 GOLGB1 golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1
1681520	0.005746627 FLJ11068 hypothetical protein FLJ11068
31225	0.01680194 BCRP2 Breakpoint cluster region protein, uterine leiomyoma, 2
1518845	7.98E-08 ESTs
590338	0.001677738 LOC51065 40S ribosomal protein S27 isoform
491706	0.017583577 Homo sapiens mRNA; cDNA DKFZp434F1622 (from clone DKFZp434F1622)
812042	0.000429178 TSC1 tuberous sclerosis 1
296702	0.01747597 DIO1 deiodinase, iodothyronine, type I
785745	1.15E-06 DXS1283E GS2 gene

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279720	5.88E-07 Homo sapiens, Similar to RIKEN cDNA 1700008D07 gene, clone MGC:9830 IMAGE:3863323, mRNA, complete cds
239877	5.74E-07 HDAC3 histone deacetylase 3
49273	0.030979591 SLC27A4 solute carrier family 27 (fatty acid transporter), member 4
758206	4.62E-06 PMS2L2 postmeiotic segregation increased 2-like 2
810446	0.011693351 KIAA1522 KIAA1522 protein
135220	0.007130449 MGC12981 hypothetical protein MGC12981
284261	0.001705915 MDS030 uncharacterized hematopoietic stem/progenitor cells protein MDS030
594627	0.000265791 FLJ11164 hypothetical protein FLJ11164
487831	0.007143248 Homo sapiens cDNA FLJ14059 fis, clone HEMBB1000573
127063	0.000920217 ESTs
1323448	3.15E-07 CRIP1 cysteine-rich protein 1 (intestinal)
742565	0.000443835 MYG1 MYG1 protein
2017756	0.005004126 MOG1 homolog of yeast MOG1
2171616	0.004755604 ITGB5 integrin, beta 5
490778	0.003255264 QP-C low molecular mass ubiquitinone-binding protein (9.5kD)
359781	0.004382798 SPTB spectrin, beta, erythrocytic (includes spherocytosis, clinical type I)
268234	2.81E-06 DMXL1 Dmx-like 1
1609616	7.68E-06 ESTs
135238	4.44E-05 ESTs
2016022	0.022592867 p25 brain-specific protein p25 alpha
741919	0.001246921 TJP3 tight junction protein 3 (zona occludens 3)
22428	0.03083658 ESTs
2017769	0.005529556 EIF4EBP1 eukaryotic translation initiation factor 4E binding protein 1
289505	1.89E-09 ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
731073	0.041342882 LOC51126 N-terminal acetyltransferase complex arid1 subunit
785766	0.004538178 LOC51321 hypothetical protein
251936	0.02996845 NSF N-ethylmaleimide-sensitive factor
810463	0.003602021 DKFZp566O084 DKFZP566O084 protein
1554430	7.94E-13 Homo sapiens cDNA FLJ10561 fis, clone NT2RP2002672
251938	0.016335389 CA14 carbonic anhydrase XIV
1032762	0.027468511 Homo sapiens mRNA; cDNA DKFZp434G2127 (from clone DKFZp434G2127)

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705274	0.027821949 DGKD diacylglycerol kinase, delta (130kD)
268240	0.019288575 FXC1 fracture callus 1 (rat) homolog
50915	0.030739747 MGC2752 hypothetical protein MGC2752
1535851	0.001352198 COX15 COX15 (yeast) homolog, cytochrome c oxidase assembly protein
429284	0.023974067 ZNF226 zinc finger protein 226
124824	1.26E-05 RPL10A ribosomal protein L10a
24032	0.001081701 CRADD CASP2 and RIPK1 domain containing adaptor with death domain
788185-2	4.38E-06 TNFRSF10B tumor necrosis factor receptor superfamily, member 10b
1517136	0.002531495 RBM8A RNA binding motif protein 8A
343731-2	0.012232736 KLF2 Kruppel-like factor 2 (lung)
111721	0.020116819 LOC51141 insulin induced protein 2
71101	3.59E-07 PROCR protein C receptor, endothelial (EPCR)
530197	0.004873141 Homo sapiens, clone MGC:5522 IMAGE:3454199, mRNA, complete cds
261706	0.010699069 Homo sapiens cDNA FLJ32056 fis, clone NTONG2001619
122147	0.040911534 ELMO2 engulfment and cell motility 2 (ced-12 homolog, C. elegans)
773617	0.038655611 UBE2D2 ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC4/5)
279752	0.038399841 DC8 DKFZP566O1646 protein
838285	7.61E-05 LOC51092 CGI-40 protein
277074	0.042882678 UNC5C unc5 (C.elegans homolog) c
2492422	0.019925171 SERPINI2 serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 2
2009904	0.015782601 FLJ11230 hypothetical protein FLJ11230
175103	7.33E-06 CELSR2 cadherin, EGF LAG seven-pass G-type receptor 2, flamingo (Drosophila) homolog
795543	0.02996845 PRDX4 peroxiredoxin 4
130845-2	0.004607159 PWP1 nuclear phosphoprotein similar to S. cerevisiae PWP1
137940	3.89E-07 GSTM3 glutathione S-transferase M3 (brain)
810486	0.014811257 EST
767069	0.012408476 Homo sapiens cDNA: FLJ21930 fis, clone HEP04301, highly similar to HSU90916 Human clone 23815
	mRNA sequence
143426	1.35E-08 ARHB ras homolog gene family, member B
826133	1.99E-08 BTBD2 BTB (POZ) domain containing 2
301122	0.016918654 ECM1 extracellular matrix protein 1
26736	0.000107772 Homo sapiens cDNA FLJ30872 fis, clone FEBRA2004293

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826138	3.22E-09	GAMT guanidinoacetate N-methyltransferase
1909163	1.63E-06	B3GNT6 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6
788334	2.20E-06	MRPL23 mitochondrial ribosomal protein L23
1518890	4.42E-08	MTL5 metallothionein-like 5, testis-specific (tesmin)
1703339	-	0.000289561 STXBP2 syntaxin binding protein 2
120561	0.025636692	KIDINS220 likely homolog of rat kinase D-interacting substance of 220 kDa
785795	4.55E-15	FLJ12910 hypothetical protein FLJ12910
2012854	0.000522332	Homo sapiens cDNA FLJ13137 fis, clone NT2RP3003150
321455	7.33E-07	SARM sterile alpha and HEAT/Armadillo motif protein, ortholog of Drosophila
179403	0.035275484	CYP2E cytochrome P450, subfamily IIE (ethanol-inducible)
126455	0.025654559	RAB5B RAB5B, member RAS oncogene family
44387	1.24E-05	ELOVL2 elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2
590390	0.013880919	MADP-1 MADP-1 protein
487882	0.01198186	DKFZP761D0211 hypothetical protein DKFZp761D0211
342720	0.00238904	KIAA0096 KIAA0096 protein
75415	5.47E-09	HINT histidine triad nucleotide-binding protein
415550	7.94E-07	Homo sapiens cDNA FLJ13598 fis, clone PLACE1009921
741954	0.016770876	Homo sapiens cDNA FLJ14656 fis, clone NT2RP2002439
759200	0.000754507	MGC4238 hypothetical protein MGC4238
1657385	0.005619887	EST
626208	0.000852377	Homo sapiens cDNA: FLJ21904 fis, clone HEP03585
1709233	0.006870641	SLC1A4 solute carrier family 1 (glutamate/neutral amino acid transporter), member 4
758266	0.01526361	THBS4 thrombospondin 4
753321	1.76E-05	KIAA0232 KIAA0232 gene product
1455842	3.72E-06	Homo sapiens cDNA: FLJ22448 fis, clone HRC09541
2028515	0.028548635	SMARCA1 SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1
1932725	0.00620659	ZNF281 zinc finger protein 281
1517171	1.50E-10	IL2RA interleukin 2 receptor, alpha
1910800	0.022735296	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
2018758	0.033107716	PEX7 peroxisomal biogenesis factor 7
469172	0.001026742	SEC22C vesicle trafficking protein

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814792	0.011398824	USP10 ubiquitin specific protease 10
415564	0.000103761	Homo sapiens, clone MGC:20208 IMAGE:3936339, mRNA, complete cds
31299	0.002342367	Homo sapiens mRNA; cDNA DKFZp76111912 (from clone DKFZp76111912)
1882481	6.16E-05	ESTs
1035359	0.012284709	FLJ22593 hypothetical protein FLJ22593
139573	0.024069066	RNPEP arginyl aminopeptidase (aminopeptidase B)
79712	0.024734713	IGF2R insulin-like growth factor 2 receptor
177827	0.005854823	SYT7 synaptotagmin VII
121533	0.043542397	WHSC1L1 Wolf-Hirschhorn syndrome candidate 1-like 1
49630	8.03E-10	CACNA1D calcium channel, voltage-dependent, L type, alpha 1D subunit
741977	0.030962737	BF B-factor, properdin
1584577	0.019525111	ESTs
1566937	0.012408476	Homo sapiens cDNA FLJ32325 fis, clone PROST2003922
726597	0.000877702	Homo sapiens cDNA FLJ32642 fis, clone SYN0V2001144
277403	0.019916149	Homo sapiens mRNA; cDNA DKFZp586D0918 (from clone DKFZp586D0918)
42018	0.000140658	KIAA1468 KIAA1468 protein
823912	0.005767924	UBL3 ubiquitin-like 3
79726	1.98E-06	ESTs, Moderately similar to T46395 hypothetical protein DKFZp4341120.1 [H.sapiens]
971212	0.002192731	HIVEP2 human immunodeficiency virus type I enhancer-binding protein 2
1507713	0.030416081	CHAD chondroadherin
418129	0.000216424	IL18BP interleukin 18 binding protein
299332	1.25E-10	KIAA0575 KIAA0575 gene product
70500	1.01E-05	TBX3 T-box 3 (ulnar mammary syndrome)
741988	0.000741391	ACY1 aminoacylase 1
769796	2.23E-08	MGC17330 hypothetical protein MGC17330
1731860	2.65E-05	GADD45B growth arrest and DNA-damage-inducible, beta
219929	0.000438842	KIAA1415 KIAA1415 protein
773674	0.005209931	RRAS2 related RAS viral (r-ras) oncogene homolog 2
712848	0.018338006	MADD MAP-kinase activating death domain
782497	1.22E-05	BC008967 hypothetical gene BC008967
843163	8.73E-06	LCP host cell factor homolog
1707667	1.78E-08	Homo sapiens cDNA FLJ31065 fis, clone HSYRA2001142

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2325804 2.47E-05 KIAA0661 | 95 kDa retinoblastoma protein binding protein
 131318 0.000194501 LOC55971 | insulin receptor tyrosine kinase substrate
 823928 0.009945291 GSTT2 | glutathione S-transferase theta 2
 824588 0.000600627 Homo sapiens cDNA FLJ32203 fis, clone PLACE6003038, weakly similar to ZINC FINGER PROTEIN 84
 2049813 0.042566514 LOC51063 | hypothetical protein
 768068 1.40E-08 DKFZP761E2110 | hypothetical protein DKFZp761E2110
 726901 0.037164505 Homo sapiens cDNA FLJ33095 fis, clone TRACH2000708
 826194 1.45E-10 SYTL2 | synaptotagmin-like 2
 1690739 0.000152094 HSPA4 | heat shock 70kD protein 4
 108864 0.000132671 OASIS | old astrocyte specifically induced substance
 23454 0.036615517 HRLP5 | H-rev107-like protein 5
 1884404 0.001613372 KIAA0285 | KIAA0285 gene product
 200954 0.001076393 EST
 1556401 0.023586705 EST
 2029503 0.041795601 ESTs
 2027900 4.84E-09 Homo sapiens cDNA FLJ12187 fis, clone MAMMA1000831
 278093 0.000144715 BRAP | BRCA1 associated protein
 823940 3.40E-05 TOB1 | transducer of ERBB2, 1
 809507 6.95E-05 FLJ20568 | hypothetical protein FLJ20568
 504763 0.019901982 SDC4 | syndecan 4 (amphiglycan, ryudocan)
 84295 0.004226757 IL1RN | interleukin 1 receptor antagonist
 262739 9.25E-05 P125 | Sec23-interacting protein p125
 725978 0.016317028 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION
 WARNING ENTRY [H:sapiens]
 714472 0.019175238 KIAA0397 | KIAA0397 gene product
 854691 0.028565804 Homo sapiens, clone MGC:17299 IMAGE:3845811, mRNA, complete cds
 288948 0.040000458 GTF2H3 | general transcription factor IIH, polypeptide 3 (34kD subunit)
 356835 0.010661105 MGC10500 | hypothetical protein MGC10500
 2016410 0.046542451 HIVEP3 | human immunodeficiency virus type I enhancer-binding protein 3
 343731 0.012195178 KLF2 | Kruppel-like factor 2 (lung)
 815794 1.67E-05 NUCB2 | nucleobindin 2
 1575008 0.000123427 WBP1 | WW domain binding protein 1

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857243	4.97E-07 RPS13 ribosomal protein S13
296030	0.027904683 Homo sapiens cDNA: FLJ20944 fis, clone ADSE01780
1882823	0.041142646 ESTs
139912	0.010208539 ESTs
202577	0.003099407 HNMT histamine N-methyltransferase
502096	0.000365845 Homo sapiens mRNA; cDNA DKFZp761K2024 (from clone DKFZp761K2024)
1404841	0.000764648 ZNF175 zinc finger protein 175
809521	0.003132437 HMT-1 beta-1,4 mannosyltransferase
666128	2.10E-05 DF D component of complement (adipsin)
770377	0.0445364 ATP6N1A ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD)
1860909	8.46E-08 Homo sapiens cDNA FLJ31136 fis, clone IMR322001029
27769	0.001838545 Homo sapiens cDNA FLJ32051 fis, clone NTONG2001428
257135	0.018649252 SLC22A4 solute carrier family 22 (organic cation transporter), member 4
83653	0.015480089 HSPC128 HSPC128 protein
345348	0.024128019 PRDM2 PR domain containing 2, with ZNF domain
1908593	0.01198186 ESTs
811803	0.001032481 SHFM3 split hand/foot malformation (ectrodactyly) type 3
813408	0.032712756 PSK-1 type I transmembrane receptor (seizure-related protein)
1568597	0.000166213 FLJ21939 hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2
39136	0.008152393 ESTs
135640	1.11E-08 STX3A syntaxin 3A
277463	8.33E-05 C18orf1 chromosome 18 open reading frame 1
827171	1.92E-05 LRRC2 leucine-rich repeat-containing 2
303109	0.028556348 P2Y5 purinergic receptor (family A group 5)
666138	0.002192122 DKFZp761J1523 hypothetical protein DKFZp761J1523
79782	0.002399976 ZNF161 zinc finger protein 161
824916	0.038531356 FLJ14511 hypothetical protein FLJ14511
788714	0.009823852 E46L like mouse brain protein E46
124143	1.91E-05 DKFZp761H1710 hypothetical protein DKFZp761H1710
2028597	0.009457359 Homo sapiens cDNA FLJ30306 fis, clone BRACE2003319
815017	2.20E-05 Homo sapiens HSPC337 mRNA, partial cds

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491053	0.000490828 ARIH2 ariadne (Drosophila) homolog 2
796598	0.031676644 LCMT leucine carboxyl methyltransferase
810873	0.014436416 SCNN1A sodium channel, nonvoltage-gated 1 alpha
752752	0.005021691 ESTs
809541	0.026417563 BCL2L2 BCL2-like 2
33267	1.26E-05 EST
813424	0.000140667 PPID peptidylprolyl isomerase D (cyclophilin D)
80338	9.63E-06 SELENBP1 selenium binding protein 1
627248	0.000251776 SBI31 SBI31 protein
755301	0.001147972 PRKCD protein kinase C, delta
52933	5.32E-10 LIV-1 LIV-1 protein, estrogen regulated
269606	0.025359903 MPG N-methylpurine-DNA glycosylase
109863	2.63E-06 EMP2 epithelial membrane protein 2
1592021	1.16E-06 HFL1 H factor (complement)-like 1
263727	1.73E-05 D5S346 DNA segment, single copy probe LNS-CAI/LNS-CAI (deleted in polyposis
295410	0.015532036 PVT1 pvt-1 (murine) oncogene homolog, MYC activator
814095	0.015960541 LTA4H leukotriene A4 hydrolase
2014856	0.007182327 HLALS major histocompatibility complex, class I-like sequence
782851	0.039199758 FLJ12799 hypothetical protein FLJ12799
2011515	0.000180794 DKFZP586B0923 DKFZP586B0923 protein
1751466	0.000262724 Homo sapiens, Similar to C-terminal modulator protein, clone MGC:29636 IMAGE:4870462, mRNA, complete cds
278430	0.0220126 KIF5C kinesin family member 5C
767475	0.046030837 PCANAP7 prostate cancer associated protein 7
767477	2.38E-09 ANKRA2 ankyrin repeat, family A (RFXANK-like), 2
179804	1.77E-06 PWP2H PWP2 (periodic tryptophan protein, yeast) homolog
126851	7.99E-08 FLJ11160 hypothetical protein FLJ11160
754376	0.034945258 ESTs, Weakly similar to Z195_HUMAN ZINC FINGER PROTEIN 195 [H.sapiens]
1592039	0.001012294 COL4A5 collagen, type IV, alpha 5 (Alport syndrome)
811843	8.82E-08 SUOX sulfite oxidase
143661-2	3.51E-07 NTN4 netrin 4
1947826	0.006003565 ITGAL integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha

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1492468	polypeptide)
684890	4.10E-08 KIAA0452 DEME-6 protein
143846	0.000308434 FLJ20274 hypothetical protein FLJ20274
135688	0.000133999 LRP2 low density lipoprotein-related protein 2
23819	0.016682884 GATA2 GATA-binding protein 2
415962	7.73E-09 ABCG1 ATP-binding cassette, sub-family G (WHITE), member 1
149735	5.02E-06 PACE4 paired basic amino acid cleaving system 4
71545	2.37E-08 CSNK1G3 casein kinase 1, gamma 3
1900362	3.96E-05 MAP4K1 mitogen-activated protein kinase kinase kinase kinase 1
325079	0.005096825 Homo sapiens chromosome 17 open reading frame 26 (C17orf26) mRNA, complete cds
767495	0.002196708 SRA1 steroid receptor RNA activator 1
897153	2.38E-09 GLI3 GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome)
589479	0.005755017 PTD009 PTD009 protein
42408	0.009372382 HPCL2 2-hydroxyphytanoyl-CoA lyase
744917	0.004066019 MGC4604 hypothetical protein MGC4604
2239290	4.06E-06 NINJ1 ninjurin 1
2018084	0.047401567 SDF1 stromal cell-derived factor 1
1700429	0.000879242 SPAK Ste-20 related kinase
810124	2.65E-09 GFRA1 GDNF family receptor alpha 1
470121	0.009454178 PAFAH1B3 platelet-activating factor acetylhydrolase, isoform lb, gamma subunit (29kD)
155227	6.56E-06 TCTA T-cell leukemia translocation altered gene
781145	4.49E-06 Homo sapiens clone 25194 mRNA sequence
127821	0.029514943 NT5M 5' nucleotidase, mitochondrial
2818432	0.018649252 ACP5 acid phosphatase 5, tartrate resistant
897164	0.004788915 EST
753743	0.013650395 CTNNA1 catenin (cadherin-associated protein), alpha 1 (102kD)
1630942	0.000185264 IL6ST interleukin 6 signal transducer (gp130, oncostatin M receptor)
1700436	0.002517943 CRN crooked neck protein (crn)
1877281	1.41E-11 ESTs
810131	0.028655076 SGCG sarcoglycan, gamma (35kD dystrophin-associated glycoprotein)
22895	0.021198683 KRT19 keratin 19
	0.004091636 INSM1 insulinoma-associated 1

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882467	1.44E-07 EST
768452	0.026097881 Homo sapiens EST from clone 491476, full insert
786096	0.048422373 APC7 anaphase-promoting complex subunit 7
768454	0.001618599 KIAA1673 KIAA1673
239568	4.44E-11 ANXA9 annexin A9
1325816	0.000370005 POLR2L polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)
266312	8.82E-07 ATP7B ATPase, Cu++ transporting, beta polypeptide (Wilson disease)
128493	0.028655076 MLH1 mutL (E. coli) homolog 1 (colon cancer, nonpolyposis type 2)
814423	0.003013488 CNNM4 cyclin M4
68636	0.036880506 MGC2477 hypothetical protein MGC2477
69293	0.004896866 PSG6 pregnancy specific beta-1-glycoprotein 6
2413337	0.00254811 SORL1 sortilin-related receptor, L(DLR class) A repeats-containing
148022	0.000123978 Homo sapiens clone Z'3-1 placenta expressed mRNA from chromosome X
1159963	0.017851437 IRF7 interferon regulatory factor 7
46716	2.46E-07 CBX4 chromobox homolog 4 (Drosophila Pc class)
470144	4.55E-06 EST
701751	0.046183854 CUTL1 cut (Drosophila)-like 1 (CCAAT displacement protein)
43090	0.002358408 H-L(3)MBT lethal (3) malignant brain tumor I(3)mbt protein (Drosophila) homolog
1860990	0.003691973 Homo sapiens cDNA FLJ32269 fis, clone PROST1000526
85624	0.025579525 C4BPA complement component 4-binding protein, alpha
592728	0.021741547 LOC51205 LPAP for lysophosphatidic acid phosphatase
1569902	7.55E-08 KIAA0556 KIAA0556 protein
744944	0.017120553 MYO6 myosin VI
132381	0.028459057 ENDOFIN endosome-associated FYVE-domain protein
1658777	0.032434932 MYO38 hypothetical brain protein my038
882484	0.028227375 CCT7 chaperonin containing TCP1, subunit 7 (eta)
725284	0.044510834 PHKG2 phosphorylase kinase, gamma 2 (testis)
1568967	0.000127809 ESTs
1571106	4.93E-06 KIAA0876 KIAA0876 protein
767819	0.02727988 KIAA0763 KIAA0763 gene product
73188	0.001353778 FLJ20259 hypothetical protein FLJ20259
2303214	0.017204034 NPPB natriuretic peptide precursor B

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145491	0.021270804 PCDH1 protocadherin 1 (cadherin-like 1)
283315	0.016037507 PGAM2 phosphoglycerate mutase 2 (muscle)
842925	0.006759973 MGC13064 hypothetical protein MGC13064
809904	0.014055609 EST
2975668	4.56E-07 RAG2 recombination activating gene 2
1848168	0.003247172 ZAK sterile-alpha motif and leucine zipper containing kinase AZK
460395	0.000805296 FLJ22625 hypothetical protein FLJ22625
1086070	0.013113828 RPH3AL rabphilin 3A-like (without C2 domains)
773308	0.032700759 Homo sapiens, clone MGC:20276 IMAGE:3844806, mRNA, complete cds
842933	0.046030837 LOC51143 dynein light chain-A
898147	1.07E-07 FLJ20417 hypothetical protein FLJ20417
50615	1.84E-06 HSPA1L heat shock 70kD protein-like 1
1456160	0.039135747 AZGP1 alpha-2-glycoprotein 1, zinc
1929165	0.043830461 ESTs, Highly similar to HXB3_HUMAN HOMEOBOX PROTEIN HOX-B3 [H.sapiens]
277848	6.68E-06 Homo sapiens cDNA FLJ13900 fis, clone THYRO1001746
743224	0.011593805 Homo sapiens cDNA FLJ11344 fis, clone PLACE1010870, moderately similar to ZINC FINGER PROTEIN
	91
302549	0.000135733 BTEB1 basic transcription element binding protein 1
1603446	0.002762432 ESTs, Weakly similar to unknown [H.sapiens]
2307514	0.00207763 MLC1 KIAA0027 protein
415229	5.28E-05 VAV3 vav 3 oncogene
75886	0.00958954 ESTs, Weakly similar to E54024 protein kinase [H.sapiens]
1601845	0.016882187 CAPRI Ca2+-promoted Ras inactivator
308437	7.30E-08 FUCA1 fucosidase, alpha-L-1, tissue
186301	7.86E-05 Homo sapiens cDNA FLJ12924 fis, clone NT2RP2004709
2524445	0.030973781 NPAS1 neuronal PAS domain protein 1
703383	3.54E-05 ESTs
129478	0.010814891 ESTs
230385	0.006373505 PIP5K2B phosphatidylinositol-4-phosphate 5-kinase, type II, beta
1915416	0.002066945 CDK7 cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)
489169	0.000415287 ESTs, Moderately similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]
796986	1.44E-06 SIG11 putative secreted protein

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811121	3.47E-05 Homo sapiens mRNA; cDNA DKFZp586B1922 (from clone DKFZp586B1922)
782147	0.011517902 KIAA0544 KIAA0544 protein
1637829	1.21E-12 ESTs
898162	0.047678928 C9orf5 chromosome 9 open reading frame 5
1500542	6.03E-08 RGS11 regulator of G-protein signalling 11
760224	0.004693782 XRCC1 X-ray repair complementing defective repair in Chinese hamster cells 1
770785	0.004763371 HMIC 1,2-alpha-mannosidase IC
488516	0.002192122 Homo sapiens, clone IMAGE:3875012, mRNA
290567	0.002138612 KBRAS1 I-kappa-B-interacting Ras-like protein 1
813813	0.017612 Homo sapiens cDNA FLJ31638 fis, clone NT2R12003556
82322	6.98E-08 RBSK ribokinase
809939	0.001725113 MAPK3 mitogen-activated protein kinase 3
430623	2.33E-05 ESTs
49303	0.033476578 PPP2R2B protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform
796996	1.40E-06 IGBP1 immunoglobulin (CD79A) binding protein 1
431286	4.10E-08 PTD002 PTD002 protein
773332	0.00185329 ITGAE integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)
866488	4.10E-08 ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
2048524	0.005767924 JAK2 Janus kinase 2 (a protein tyrosine kinase)
61061	0.018883013 FBNP3 formin-binding protein 3
357120	0.000238959 Homo sapiens, clone IMAGE:3538007, mRNA, partial cds
1560723	0.029910221 HOXB3 homeo box B3
1412344	0.007631302 GP2 glycoprotein 2 (zymogen granule membrane)
809944	0.00289345 KIAA0310 KIAA0310 gene product
1607755	7.06E-05 HSPC141 HSPC141 protein
1460075	0.042644552 PIN1 protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1
120271	0.004728263 MGC4692 hypothetical protein MGC4692
1637843	0.001725113 HSPA5 heat shock 70kD protein 5 (glucose-regulated protein, 78kD)
501868	0.000425258 RAI2 retinoic acid induced 2
308466	6.75E-05 LOC51128 GTP-binding protein Sara
362755	0.005875967 PRKAG1 protein kinase, AMP-activated, gamma 1 non-catalytic subunit
362756	0.020883314 KIAA1164 hypothetical protein KIAA1164

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1604423	0.013359346 ESTs
243800	0.017125244 RYBP RING1 and YY1 binding protein
731104	3.25E-07 ESTs
266389	8.87E-09 SLC16A6 solute carrier family 16 (monocarboxylic acid transporters), member 6
502818	2.33E-06 ARHA ras homolog gene family, member A
1636111	0.019413865 HNRPU heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
1570502	0.017495868 Homo sapiens cDNA FLJ12936 fis, clone NT2RP2005018
251682	1.50E-06 TINF2 TERF1 (TRF1)-interacting nuclear factor 2
773353	0.026514552 Homo sapiens cDNA FLJ31753 fis, clone NT2RI2007468
111469	5.71E-05 Homo sapiens clone IMAGE:111469 mRNA sequence
40100	0.029910221 Homo sapiens, clone MGC:18084 IMAGE:4150952, mRNA, complete cds
454173	0.003570072 WDR7 WD repeat domain 7
842980	1.87E-06 DRG1 developmentally regulated GTP-binding protein 1
454175	0.009321073 HIT-17 PKC1-1-related HIT protein
1609372	0.008647658 RIPK3 receptor-interacting serine-threonine kinase 3
302591	3.97E-10 ARHH ras homolog gene family, member H
66317	0.029073646 H1F2 H1 histone family, member 2
201282	0.030274401 DKFZP434N126 DKFZP434N126 protein
472103	0.005357267 SHOC2 soc-2 (suppressor of clear, C.elegans) homolog
795288	0.017376841 USP4 ubiquitin specific protease 4 (proto-oncogene)
2016869	0.006544656 KIAA1131 KIAA1131 protein
811162	0.024982615 FMOD fibromodulin
1910516	0.000122585 ESTs
491486	0.000923428 LOC51578 adrenal gland protein AD-004
1558473	0.020974589 ESTs
1947144	0.028543112 ESTs
757327	0.01394813 LOC51249 hypothetical protein
429322	0.008351255 Homo sapiens, clone IMAGE:3447394, mRNA, partial cds
868400	0.013032007 QARS glutamyl-tRNA synthetase
50675	2.78E-08 KIAA0423 KIAA0423 protein
143169	4.17E-06 Homo sapiens, clone IMAGE:3881549, mRNA
823615	0.014557615 Homo sapiens cDNA: FLJ21245 fis, clone COL01184

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1917063	0.00188129 Homo sapiens, clone MGC:15400 IMAGE:4040570, mRNA, complete cds
1455566	0.000327751 ADORA3 adenosine A3 receptor
813854	0.028548635 PURA purine-rich element binding protein A
795296	6.64E-07 CCNH cyclin H
725649	3.06E-05 NFATC4 nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4
49344	0.000860578 KIAA0350 KIAA0350 protein
415287	0.023418315 ESTs
149058	0.042155684 Homo sapiens cDNA FLJ10174 fis, clone HEMBA1003959
2306919	4.44E-05 SLC35A3 solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3
2072768	0.044848397 NCOA3 nuclear receptor coactivator 3
757337	6.19E-07 ESTs
1686547	0.039985007 ESTs
74119-2	0.002954849 SNRPN small nuclear ribonucleoprotein polypeptide N
489509	0.031251603 Homo sapiens mRNA; cDNA DKFZp564L0822 (from clone DKFZp564L0822)
1870049	0.005305054 DDO D-aspartate oxidase
683569	0.000182323 ITPR1 inositol 1,4,5-triphosphate receptor, type 1
50685	0.048777689 KIAA1414 KIAA1414 protein
611239	0.000438876 Homo sapiens cDNA: FLJ22361 fis, clone HRC06524, highly similar to HSU15426 Human anonymous mRNA sequence with CCA repeat region
261472	0.017638942 ORF1-FL49 putative nuclear protein ORF1-FL49
279800	5.50E-05 SLMAP sarcolemma associated protein
49351	0.004160342 HSSEXGENE SEX gene
49354	1.84E-06 ANK2 ankyrin 2, neuronal
773381	0.000877702 NAPA N-ethylmaleimide-sensitive factor attachment protein, alpha
714159	0.030468197 Homo sapiens cDNA FLJ32185 fis, clone PLACE6001925
754002	0.040830931 DKK3 dickkopf (Xenopus laevis) homolog 3
51631	6.17E-07 DKFZP586B1621 DKFZP586B1621 protein
289287	0.017659789 Homo sapiens mRNA; cDNA DKFZp586J101 (from clone DKFZp586J101)
301963	0.001486067 SNX11 sorting nexin 11
742641	0.017924982 MGC5540 hypothetical protein MGC5540
823634	0.000159834 ESTs
564621	0.011672024 SERPINI1 serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1

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814815	0.00048204 EST
796255	6.94E-06 MRPS14 mitochondrial ribosomal protein S14
344073	7.94E-08 Homo sapiens cDNA FLJ131763 fis, clone NT2RI2007827
1557841	0.001309802 ESTs
2020772	0.000172997 TM7SF2 transmembrane 7 superfamily member 2
1637893	1.84E-06 Homo sapiens, clone MGC:9575 IMAGE:3879368, mRNA, complete cds
753071	0.005767924 Homo sapiens cDNA: FLJ22528 fis, clone HRC12825
42827	0.003388822 Homo sapiens cDNA FLJ131604 fis, clone NT2RI2002699
22500	0.000613835 ESTs
841287	0.001159126 GNPAT glyceronephosphate O-acyltransferase
301976	0.000553787 PPP3CC protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma)
785840	0.028503208 SEC24D SEC24 (S. cerevisiae) related gene family, member D
814826	0.000212133 ESTs
725672	0.030333035 Homo sapiens, Similar to transducin (beta)-like 3, clone MGC:8613 IMAGE:2961321, mRNA, complete cds
784105	0.03689826 ESTs
812143	0.009962681 FLRT3 fibronectin leucine rich transmembrane protein 3
1948122	0.0285188 FLJ10450 hypothetical protein FLJ10450
1877697	0.000466212 ESTs
1901735	0.004586404 RPP14 ribonuclease P (14kD)
454503	1.11E-05 Homo sapiens, clone IMAGE:3346451, mRNA, partial cds
80798	0.002033157 ITM2B integral membrane protein 2B
594724	0.001075123 YR-29 hypothetical protein
681992	0.038338214 Homo sapiens cDNA FLJ13384 fis, clone PLACE1001062, highly similar to Homo sapiens mRNA for lysine-ketoglutarate reductase/saccharopine dehydrogenase
487932	5.59E-09 SYTL2 synaptotagmin-like 2
868441	0.003083769 FLJ20727 hypothetical protein FLJ20727
729964	0.004902138 SMPD1 sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)
345034	0.017833089 SCYB14 small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK)
884480	0.022202501 COX7C cytochrome c oxidase subunit VIIc
823655	3.25E-08 AD036 AD036 protein
823659	1.46E-06 FYCO1 FYVE and coiled-coil domain containing 1

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298417	1.30E-14	TFF3 trefoil factor 3 (intestinal)
2063982	2.33E-07	KCNK6 potassium channel, subfamily K, member 6 (TWIK-2)
44443	0.042068695	SCYE1 small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)
838366	1.25E-05	HMGCL 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)
754033	7.67E-06	LZTFL1 leucine zipper transcription factor-like 1
754034	0.001228195	THPO thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)
897593	1.41E-06	KIAA1548 KIAA1548 protein
770074	0.00038924	PRRG2 proline-rich Gla (G-carboxyglutamic acid) polypeptide 2
753092	1.98E-06	EST
1631238	0.007429314	KIAA1483 KIAA1483 protein
415610	0.000498483	FLJ22402 hypothetical protein FLJ22402
2018808	0.038787441	PRCP prolylcarboxypeptidase (angiotensinase C)
823661	0.000706071	Homo sapiens cDNA FLJ31768 fis, clone NT2RI2007891, moderately similar to DMR-N9 PROTEIN
486208	0.000218364	TGFB3 transforming growth factor, beta 3
487948	0.000529233	Homo sapiens cDNA: FLJ22566 fis, clone HSI01980
67318	0.012702024	Homo sapiens, Similar to RIKEN cDNA 0610039G24 gene, clone MGC:15403 IMAGE:4126342, mRNA, complete cds
83358	1.39E-11	ESTs
1583673	2.86E-06	ESTs, Weakly similar to KIAA0351 [H.sapiens]
784126	0.009372382	TST thiosulfate sulfurtransferase (rhodanase)
366315	0.024091716	Homo sapiens, clone MGC:20500 IMAGE:4053084, mRNA, complete cds
2366057	0.000958877	CDH12 cadherin 12, type 2 (N-cadherin 2)
47795	0.01192016	ZNF161 zinc finger protein 161
51672	9.79E-05	ARRB1 arrestin, beta 1
124922	0.000642521	SZF1 KRAB-zinc finger protein SZF1-1
193916	0.030979591	RHBG Rhesus blood group, B glycoprotein
1925280	5.88E-07	NPR2L homologous to yeast nitrogen permease (candidate tumor suppressor)
266747	0.034115322	Homo sapiens, Similar to RIKEN cDNA 2010001O09 gene, clone MGC:21387 IMAGE:4471592, mRNA, complete cds
429387	0.001030569	CHN2 chimera (chimaerin) 2
345055	9.76E-05	ESTs, Highly similar to LB4D_HUMAN NADP-DEPENDENT LEUKOTRIENE B4 12-

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HYDROXYDEHYDROGENASE [H.sapiens]	
345056	0.000129022 KIAA1404 KIAA1404 protein
258589	0.000383745 REL v-rel avian reticuloendotheliosis viral oncogene homolog
190295	2.00E-05 FLJ23590 hypothetical protein FLJ23590
782537	0.045949613 Homo sapiens cDNA FLJ30428 fis, clone BRACE2008941
1554549	1.10E-06 HAGH hydroxyacyl glutathione hydrolase
143519	0.023557456 FKBP2 FK506-binding protein 2 (13kD)
838389	1.40E-08 UNC119 unc119 (C.elegans) homolog
184022	0.010544493 APBB1 amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65)
840664	0.000657157 EST
203240	3.98E-06 DAB2 disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)
300271	0.003251584 SAS10 disrupter of silencing 10
131070	0.00841697 KIAA0670 KIAA0670 protein/acinus
196189	1.68E-07 CYB5 cytochrome b-5
453599	0.001069723 DKFZP564F1123 DKFZP564F1123 protein
823682	0.026331677 KIAA0710 KIAA0710 gene product
784140	0.003891255 WDR11 WD40 repeat domain 11 protein
31366	0.011252089 MYT1 myelin transcription factor 1
1558832	0.003860708 MAT2B methionine adenosyltransferase II, beta
742695	3.48E-07 Homo sapiens cDNA FLJ31534 fis, clone NT2RI2000671
726658	8.52E-08 NME3 non-metastatic cells 3, protein expressed in
823688	0.045171023 MAN1A1 mannosidase, alpha, class 1A, member 1
2322223	2.50E-05 SNRPA small nuclear ribonucleoprotein polypeptide A
866874	8.19E-08 HNRPH2 heterogeneous nuclear ribonucleoprotein H2 (H')
250313	0.000892123 ESTs
685516	2.07E-10 GPCR150 putative G protein-coupled receptor
288683	0.00367697 ESTs
461761	1.58E-05 ANG angiogenin, ribonuclease, RNase A family, 5
758347	6.94E-05 SLC2A10 solute carrier family 2 (facilitated glucose transporter), member 10
1650927	0.004105721 DKFZp547E052 hypothetical protein DKFZp547E052
128143	2.88E-06 PON1 paraoxonase 1
753404	0.037494688 KIAA0887 KIAA0887 protein

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214751	0.000487816	Homo sapiens, clone MGC:12617 IMAGE:2964706, mRNA, complete cds
1694775	0.000354216	EST
277185	0.000614717	PRO0461 PRO0461 protein
2432360	0.006342148	BSN bassoon (presynaptic cytomatrix protein)
1609748	2.16E-06	MGC10882 hypothetical protein MGC10882
1915824	0.003398986	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
2067500	4.36E-11	LDB3 LIM domain binding 3
823691	4.27E-08	CCNG2 cyclin G2
1895664	0.026431801	PRO2198 hypothetical protein PRO2198
243100	1.01E-06	ACADSB acyl-Coenzyme A dehydrogenase, short/branched chain
784150	3.38E-10	RAB31 RAB31, member RAS oncogene family
785890	0.032434657	Homo sapiens cDNA FLJ14030 fis, clone HEMBA1004086
784154	0.014124729	ESTs, Highly similar to unnamed protein product [H.sapiens]
767170	0.026562375	LOC51606 CGI-111 protein
767171	5.14E-05	FLJ20015 hypothetical protein
812196	0.000269329	UGCG UDP-glucose ceramide glucosyltransferase
145132	0.017780719	MPDU1 mannose-6-phosphate utilization defect 1
767176	0.003072281	TNFSF13 tumor necrosis factor (ligand) superfamily, member 13
855385	0.008682257	CLN2 ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease)
843224	1.13E-05	DSCR2 Down syndrome critical region gene 2
283751	0.032429761	CORT cortistatin
233349	0.000116838	FLJ10761 hypothetical protein FLJ10761
1536925	6.56E-06	PDPK1 3-phosphoinositide dependent protein kinase-1
771058	1.40E-08	CISH cytokine inducible SH2-containing protein
1323591	1.62E-07	SERPINA5 serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5
826245	1.66E-05	LOC54505 hypothetical protein
1895672	9.67E-05	ESTs, Weakly similar to S57447 HPBR11-7 protein [H.sapiens]
840687	0.004816698	MUC1 mucin 1, transmembrane
80050	0.036628745	FLJ23153 likely ortholog of mouse tumor necrosis-alpha-induced adipose-related protein
82738	2.39E-09	DNASE1L3 deoxyribonuclease I-like 3
503866	0.011391526	SPA17 sperm autoantigenic protein 17

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1027283	0.009413465 ESTs
147826	0.003162135 ESTs
38213	0.000167261 FLJ22174 hypothetical protein FLJ22174
1502566	1.61E-05 ESTs, Weakly similar to T21437 hypothetical protein F26H9.4 - <i>Caenorhabditis elegans</i> [C.elegans]
754080	0.012652328 ICAM3 intercellular adhesion molecule 3
267725	5.65E-05 BC-2 putative breast adenocarcinoma marker (32kD)
1703455	0.004124332 EDG2 endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2
344432	0.001735764 MGST2 microsomal glutathione S-transferase 2
2015517	6.88E-09 FLJ22237 hypothetical protein FLJ22237
813154	0.046806631 NFIA nuclear factor I/A
322511	4.76E-08 Homo sapiens mRNA; cDNA DKFZp564D1462 (from clone DKFZp564D1462)
814899	0.001468215 BNIP3L BCL2/adenovirus E1B 19kD-interacting protein 3-like
160532	0.004538178 ESTs, Weakly similar to JX0331 laurate omega-hydroxylase [H.sapiens]
784178	1.98E-06 Homo sapiens mRNA; cDNA DKFZp586M0723 (from clone DKFZp586M0723)
1536941	0.000449552 ESTs, Moderately similar to ALU2_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
841641	4.35E-06 CCND1 cyclin D1 (PRAD1: parathyroid adenomatosis 1)
843248	0.001755052 VAMP3 vesicle-associated membrane protein 3 (cellubrevin)
127519	2.29E-08 POH1 26S proteasome-associated pad1 homolog
43849	0.001286711 ESTs
815847	0.038913997 C11orf5 chromosome 11 open reading frame 5
261852	0.001941321 ESTs
2306221	1.79E-12 WNT10B wingless-type MMTV integration site family, member 10B
813165	0.003482886 PGRMC2 progesterone receptor membrane component 2
811565	1.51E-05 KIAA1694 KIAA1694 protein
726699	4.73E-07 Homo sapiens, clone MGC:9889 IMAGE:3868330, mRNA, complete cds
1555536	3.04E-06 LGP1 likely ortholog of mouse D11lgp1
771084	0.000459658 BECN1 beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)
526757	1.84E-05 CCND1 cyclin D1 (PRAD1: parathyroid adenomatosis 1)
42118	8.31E-05 P2RX4 purinergic receptor P2X, ligand-gated ion channel, 4
28475	0.001063475 CRYZ crystallin, zeta (quinone reductase)
841655	1.97E-05 RBBP2 retinoblastoma-binding protein 2

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1632247	0.001096449 FLJ23436 hypothetical protein FLJ23436
753447	0.014351752 DDB2 damage-specific DNA binding protein 2 (48kD)
280444	0.000352001 KIAA0608 KIAA0608 protein
745289	0.029910221 PNAS-127 PNAS-127 protein
502153	0.005704405 Homo sapiens, clone MGC:16377 IMAGE:3936171, mRNA, complete cds
378824	0.000177644 HSPC009 HSPC009 protein
784190	0.000123726 Homo sapiens, Similar to RIKEN cDNA 553060119 gene, clone MGC:3854028, mRNA, complete cds
70606	0.022570057 ESTs
854763	9.74E-07 MGC20702 hypothetical protein MGC20702
2284473	0.01376248 ZK1 Kruppel-type zinc finger (C2H2)
1588973	0.000173284 IMAGE3451454 hypothetical protein IMAGE3451454
26883	1.17E-07 PKIB protein kinase (cAMP-dependent, catalytic) inhibitor beta
796643	0.012443564 NEBL nebulin
877636	2.16E-05 DCTN4 dynactin 4 (p62)
2017144	0.002872765 LOC51093 CGI-41 protein
1048586	0.009471574 BMI1 murine leukemia viral (bmi-1) oncogene homolog
813183	0.01280152 AZU1 azurocidin 1 (cationic antimicrobial protein 37)
486288	0.012126378 Homo sapiens clone CDABP0028 mRNA sequence
811582	1.35E-07 GOLPH2 golgi phosphoprotein 2
838732	1.49E-05 LOC51596 divalent cation tolerant protein CUTA
813189	2.96E-05 EST
811585	0.000116498 HD huntingtin (Huntington disease)
1558895	0.041918884 PGAM2 phosphoglycerate mutase 2 (muscle)
208531	5.51E-06 FLJ20551 hypothetical protein FLJ20551
150003	1.31E-07 FLJ13187 phafin 2
293569	9.71E-05 C1orf21 chromosome 1 open reading frame 21
25154	0.004517557 PLAT plasminogen activator, tissue
824692	4.04E-06 SEL1L sel-1 (suppressor of lin-12, C.elegans)-like
841679	0.00456714 SIP2-28 calcium and integrin binding protein (DNA-dependent protein kinase interacting protein)
1908666	0.018949143 ZNF79 zinc finger protein 79 (pT7)
1558108	0.000693345 ABCC8 ATP-binding cassette, sub-family C (CFTR/MRP), member 8

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810937	0.001309095 TPST2 tyrosylprotein sulfotransferase 2
1473914	0.00225716 C21orf15 chromosome 21 open reading frame 15
897971	0.001037841 COPB coatomer protein complex, subunit beta
489922	0.006100942 AKAP10 A kinase (PRKA) anchor protein 10
754417	0.038568449 Homo sapiens mRNA; cDNA DKFZp586H021 (from clone DKFZp586H021)
1456937	0.000129703 OVGPI oviductal glycoprotein 1, 120kD (mucin 9, oviductin)
841685	0.03461124 SID6-306 inorganic pyrophosphatase
796663	0.002337587 DRIP78 dopamine receptor interacting protein
267778	0.004321341 ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]
1896676	1.24E-06 Homo sapiens cDNA: FLJ22113 fis, clone HEP18418
814145	2.06E-05 JTB jumping translocation breakpoint
1637504	0.017405243 EST
296123	0.009311435 Homo sapiens PRO1851 mRNA, complete cds
48033	9.67E-07 ESTs
810947	0.006557959 NUDE1 LIS1-interacting protein NUDE1, rat homolog
810948	0.001616352 TRAP240 thyroid hormone receptor-associated protein, 240 kDa subunit
454908	0.00286005 CGA glycoprotein hormones, alpha polypeptide
283023	0.010085994 CX3CR1 chemokine (C-X3-C) receptor 1
897982	0.009962681 EIF3S8 eukaryotic translation initiation factor 3, subunit 8 (110kD)
380057	0.000839497 APPBP2 amyloid beta precursor protein (cytoplasmic tail)-binding protein 2
179572	3.91E-10 Homo sapiens cDNA FLJ14227 fis, clone NT2RP3004095
841695	0.008164837 CG018 hypothetical gene CG018
30793	0.002706225 PEX11B peroxisomal biogenesis factor 11B
23579	0.010974699 Homo sapiens clone Z3579 mRNA sequence
1914168	0.045350687 FLJ20558 hypothetical protein FLJ20558
1637516	0.009609456 GS2NA nuclear autoantigen
1635913	0.041470052 LNX multi-PDZ-domain-containing protein
502198	0.00087773 PPP1R3C protein phosphatase 1, regulatory (inhibitor) subunit 3C
1520559	0.031251603 ESTs
294537	2.82E-08 RAB17 RAB17, member RAS oncogene family
1899230	0.047956858 H.sapiens mRNA for metallothionein isoform 1R
488202	6.46E-07 Homo sapiens cDNA FLJ31235 fis, clone KIDNE2004681, moderately similar to Mus musculus

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271670	0.012020011	peroxisomal long chain acyl-CoA thioesterase 1b (Pte1b) gene
430318	0.002444659	TNFSF12 tumor necrosis factor (ligand) superfamily, member 12
2284803	0.002768702	PVALB parvalbumin
470964	0.002768702	SCAMP1 secretory carrier membrane protein 1
	1.58E-07	GALNT6 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)
196570	0.000194501	MGC2747 hypothetical protein MGC2747
754443	0.023018366	Homo sapiens cDNA FLJ13771 fis, clone PLACE4000270
1536215	0.008360311	GALNAC4S-6ST B cell RAG associated protein
700836	0.001618877	ZNF19 zinc finger protein 19 (KOX 12)
1553996	2.38E-05	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
50339	1.99E-07	ESTs, Moderately similar to hypothetical protein [H.sapiens]
2103000	0.019869834	ESTs
25194	0.000197727	Homo sapiens clone 25194 mRNA sequence
1523116	0.000863455	NESH NESH protein
1593849	0.013132955	PDE4A phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2)
813518	0.001929727	ESTs
2138030	0.0247432	KCNS3 potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3
66787	0.037494688	TRIP3 thyroid hormone receptor interactor 3
215000	1.30E-06	VIPR1 vasoactive intestinal peptide receptor 1
197525	0.009040685	FMO5 flavin containing monooxygenase 5
826622	1.28E-06	KIAA0430 KIAA0430 gene product
291216	0.011893765	CETN2 centrin, EF-hand protein, 2
2460159	0.040000458	TNK1 tyrosine kinase, non-receptor, 1
1410444	0.002729944	AREG amphiregulin (schwannoma-derived growth factor)
882511	0.000981881	M17S2 membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen CA125)
214068	4.60E-25	GATA3 GATA-binding protein 3
417637	0.02117967	KIAA1276 KIAA1276 protein
111150	0.008720987	LNK multi-PDZ-domain-containing protein
1558151	3.27E-06	BATF basic leucine zipper transcription factor, ATF-like
2052113	6.56E-06	FLJ10903 hypothetical protein FLJ10903

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321945	0.000909807 ESTs	
810987	1.62E-06 MBC3205 hypothetical protein MBC3205	
26152	0.011314426 KIAA1557 KIAA1557 protein	
1534633	0.019925171 MGC2479 hypothetical protein MGC2479	
788632	9.78E-06 PLAB prostate differentiation factor	
725321	1.53E-22 ESR1 estrogen receptor 1	
85384	0.000225058 ATP11 hypothetical protein FLJ22351	
2018158	0.019146124 ESTs	
814191	0.04385949 KIAA0295 KIAA0295 protein	
487297	0.001907323 CAP2 adenyl cyclase-associated protein 2	
730942	0.002682409 DECR2 2,4-dienoyl CoA reductase 2, peroxisomal	
502518	0.000152832 LAMB2 laminin, beta 2 (laminin S)	
811937	0.015875339 SNX9 sorting nexin 9	
278531	7.09E-07 COX6C cytochrome c oxidase subunit VIc	
1558166	1.96E-07 ESTs, Moderately similar to AF072733 1 putative secreted protein [H.sapiens]	
137370	0.007518112 ESTs	
704062	5.44E-05 SIRT3 sirtuin (silent mating type information regulation 2, S.cerevisiae, homolog) 3	
593431	8.35E-13 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1287006	
595037	0.008509083 RAI3 retinoic acid induced 3	
240966	0.012397017 PCBP2 poly(rC)-binding protein 2	
754474	0.016470796 ESTs	
344820	0.021127692 KIF3A kinesin family member 3A	
486641	0.000140204 MOCS2 molybdenum cofactor synthesis 2	
1898619	7.34E-10 MGC15737 hypothetical protein MGC15737	
450673	7.31E-05 SPATA2 spermatogenesis associated 2	
1917837	0.034946932 FLJ11838 hypothetical protein FLJ11838	
85394	0.01312499 PPAP2B phosphatidic acid phosphatase type 2B	
345487	0.035143688 Homo sapiens, clone MGC:23280 IMAGE:4637504, mRNA, complete cds	
811944	0.045490722 ESTs	
786169	0.003709448 FLJ11088 hypothetical protein FLJ11088	
376516	7.09E-07 LRBA vesicle trafficking, beach and anchor containing	
70692	0.025359903 SERPINB2 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2	

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147147	0.005871121 ESTs
1563792	0.001655476 LOC51333 mesenchymal stem cell protein DSC43
1687976	0.005209931 SIL1 endoplasmic reticulum chaperone SIL1, homolog of yeast
1898625	0.00480123 ANKTM1 ankyrin-like with transmembrane domains 1
130845	0.016285335 PWP1 nuclear phosphoprotein similar to S. cerevisiae PWP1
1947933	0.032222366 FLJ12800 hypothetical protein FLJ12800
296190	0.000356685 KIAA0321 KIAA0321 protein
588915	0.001292252 IFI27 interferon, alpha-inducible protein 27
50383	0.019695801 KIAA1598 KIAA1598 protein
2346188	0.037722909 PNKP polynucleotide kinase 3'-phosphatase
41569	2.04E-09 FLJ12650 hypothetical protein FLJ12650
868119	0.000560528 LOC57117 hypothetical nuclear factor SBB122
815167	0.001112368 PLEKHA3 pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3
342164	0.037052367 FLJ14486 hypothetical protein FLJ14486
377193	0.024734713 LOC54505 hypothetical protein
1492587	0.01198186 Homo sapiens, Similar to RAB37, member of RAS oncogene family, clone MGC:21391 IMAGE:4520191, mRNA, complete cds
276962	0.000184101 LOC57149 hypothetical protein A-211C6.1
143966	0.044999609 2-Sep septin 6
1707078	0.023623028 LOC51646 CGI-127 protein
108265	0.027824136 Homo sapiens, clone MGC:21518 IMAGE:3900532, mRNA, complete cds
785535	0.029849385 DDXBP1 DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1
1415720	0.032290985 EST
243549	1.35E-05 MYB v-myb avian myeloblastosis viral oncogene homolog
1031592	9.21E-07 KIF9 kinesin family member 9
1460110	0.026915103 PSMB5 proteasome (prosome, macropain) subunit, beta type, 5
285798	1.41E-06 ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens]
176606	0.032429761 NELL2 nel (chicken)-like 2
272694	0.037494688 C1orf9 chromosome 1 open reading frame 9
814528	4.69E-05 p53DINP1 p53-inducible p53DINP1
342181	1.41E-11 BCL2 B-cell CLL/lymphoma 2

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813584	0.028503208 PA26 p53 regulated PA26 nuclear protein
813585	0.004222762 XAP4 HBV associated factor
2011660	0.005969978 DKFZp434K1210 hypothetical protein DKFZp434K1210
248499	0.010004815 AF5Q31 ALL1 fused gene from 5q31
898221	5.65E-05 NR4A2 nuclear receptor subfamily 4, group A, member 2
898222	0.000998114 ATP12 homolog of yeast ATP12
770840	0.012755509 AVIL advillin
1640821	3.60E-08 Homo sapiens, clone IMAGE:3899073, mRNA, partial cds
470249	0.000754806 ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
491486-2	0.002434509 LOC51578 adrenal gland protein AD-004
143989	0.020286058 KIAA1340 KIAA1340 protein
665658	0.000136335 MSX2 msh (Drosophila) homeo box homolog 2
1762326	4.41E-05 ESTs
74223	0.00021037 HTPAP HTPAP protein
344988-2	2.10E-05 EST
768570	3.26E-12 FLJ11280 hypothetical protein FLJ11280
858387	0.000198568 MGC4767 hypothetical protein MGC4767
1030953	0.007749864 LOC80298 transcription termination factor-like protein
365060	0.000392359 RAB11A RAB11A, member RAS oncogene family
283413	0.004226861 LRDD leucine-rich and death domain containing
1709786	0.026592724 TRPS1 trichorhinophalangeal syndrome I
143995	0.025539645 Homo sapiens mRNA from chromosome 5q21-22, clone:FBR89
1526826	4.26E-06 HOXB2 homeo box B2
140655	0.004076409 dJ453C12.4.1 similar to RIKEN cDNA 2610042O14 gene (M. musculus)
322160-2	0.023425543 PTEN phosphatase and tensin homolog (mutated in multiple advanced cancers 1)
814546	0.019909138 ESTs, Highly similar to PCID1_HUMAN CYTOHESIN 1 [H.sapiens]
130895	8.00E-10 Homo sapiens cDNA: FLJ22930 fis, clone KAT07255
725394	0.005095011 CLPX ClpX (caseinolytic protease X, E. coli) homolog
504187	4.31E-05 ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION
	WARNING ENTRY [H.sapiens]
725395	0.037816121 UBE2L6 ubiquitin-conjugating enzyme E2L 6
502585	0.001007942 RAB18 RAB18, member RAS oncogene family

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782385-2	0.011252089 DKFZP566D193 DKFZP566D193 protein
132381-2	1.73E-05 ENDOFIN endosome-associated FYVE-domain protein
154707	0.02165445 MPV17 MpV17 transgene, murine homolog, glomerulosclerosis
163528	0.000751027 PALM paralemmin
306924	6.86E-07 KIAA0222 KIAA0222 gene product
296529	0.027905446 KIAA1504 KIAA1504 protein
470261	7.82E-05 SMA5 SMA5
1709791	9.70E-08 BAIAP1 BAI1-associated protein 1
110578	0.000133284 ESTs
1457205	4.94E-05 Homo sapiens cDNA FLJ20525 fis, clone KAT10610
1708055	0.026818494 GOV glioblastoma overexpressed
358936	4.04E-06 ESTs, Weakly similar to T2D3_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]
1626409	0.005619887 AP2A1 adaptor-related protein complex 2, alpha 1 subunit
770866	0.042071414 Homo sapiens, clone MGC:9709 IMAGE:3850147, mRNA, complete cds
347434	0.000306027 SC65 nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein
795330	0.043246672 NR1D1 nuclear receptor subfamily 1, group D, member 1
347436	0.000531118 GSTTlp28 glutathione-S-transferase like; glutathione transferase omega
357996	0.024330122 FLJ20156 hypothetical protein FLJ20156
770869	0.002110844 MGC2592 hypothetical protein MGC2592
126229	0.007870589 MGC12760 hypothetical protein MGC12760
130104	0.025309814 Homo sapiens, clone IMAGE:3352566, mRNA, partial cds
269788	0.001755224 SEDLP spondyloepiphyseal dysplasia, late, pseudogene
785571	0.000352444 DNAJL1 hypothetical protein similar to mouse DnaJ1
325515	2.23E-08 FLJ10980 hypothetical protein FLJ10980
868168	6.52E-05 SPRR2A small proline-rich protein 2A
785574	0.000174826 SNX1 sorting nexin 1
199505	0.000661388 SENP7 sentrin/SUMO-specific protease
46843	0.012102208 SLI neuronal Shc adaptor homolog
898251	0.020270563 FLJ20727 hypothetical protein FLJ20727
1950130	0.009056557 Homo sapiens cDNA FLJ14115 fis, clone MAMMA1001760
739450	0.002041876 LASS2 longevity assurance (LAG1, S. cerevisiae) homolog 2

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781295	0.004349202 SCAD-SRL peroxisomal short-chain alcohol dehydrogenase
127970	0.029073646 Homo sapiens cDNA FLJ13557 fis, clone PLACE1007737
772477	0.008407492 Homo sapiens, clone MGC:19570 IMAGE:3942960, mRNA, complete cds
241988	7.09E-06 WDR6 WD repeat domain 6
795342	0.026143501 ESTs
753897	3.10E-07 AMFR autocrine motility factor receptor
786525	0.020146808 KIAA1917 KIAA1917 protein
812968	0.00014351 PTPRN2 protein tyrosine phosphatase, receptor type, N polypeptide 2
1559198	0.000278805 Homo sapiens cDNA FLJ14923 fis, clone PLACE1008244, weakly similar to VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1
141623	0.037935139 LOC51056 leucine aminopeptidase
366039	2.23E-05 ESTs, Weakly similar to ABP2_HUMAN ENDOTHELIAL ACTIN-BINDING PROTEIN [H.sapiens]
2054896	0.007810967 FLJ21669 hypothetical protein FLJ21669
969495	0.001699546 TIGA1 TIGA1
786530	0.001147277 FLJ23027 hypothetical protein FLJ23027
82421	0.010334304 CD44 CD44 antigen (homing function and Indian blood group system)
1892025	0.019936342 MGC13170 hypothetical protein MGC13170
343174	1.92E-05 Homo sapiens cDNA FLJ31204 fis, clone KIDNE2003305, weakly similar to PUTATIVE AMIDASE AF1954 (EC 3.5.1.4)
769552	0.001219419 LENG4 leukocyte receptor cluster (LRC) member 4
1409509	0.007517038 TNNT1 troponin T1, skeletal, slow
785595	0.033081925 STE sulfotransferase, estrogen-preferring
139354	8.04E-09 HSPC195 hypothetical protein
1493596	0.018150022 VLGR1 very large G protein-coupled receptor 1
898276	0.000107772 HSMNP1 uncharacterized hypothalamus protein HSMNP1
788141	0.000137025 XPA xeroderma pigmentosum, complementation group A
3208314	0.017495868 GPR27 G protein-coupled receptor 27
2164248	0.041777908 HMG20B high-mobility group 20B
502909	0.000155359 KIAA0326 KIAA0326 protein
812989	0.039337098 DJ1141E15.2 hypothetical protein dJ1141E15.2
1556957	0.013797398 Homo sapiens cDNA FLJ32647 fis, clone SYNOV2001374, moderately similar to ZINC FINGER PROTEIN 134

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897625	0.024870477 KIAA0532 KIAA0532 protein
701112	0.000600597 XPC xeroderma pigmentosum, complementation group C
179212	4.11E-11 ESTs, Moderately similar to T12539 hypothetical protein DKFZp434J154.1 [H.sapiens]
1539977	0.001651449 SLC27A1 solute carrier family 27 (fatty acid transporter), member 1
824354	0.004173726 GRILF1 glucocorticoid receptor DNA binding factor 1
327150	0.033503623 DOCK1 dedicator of cyto-kinesis 1
487697	0.001175473 CROT carnitine O-octanoyltransferase
1603583	3.02E-05 SH3BGR1 SH3 domain binding glutamic acid-rich protein like
769571	0.000117954 SREBF1 sterol regulatory element binding transcription factor 1
510794	0.00135873 MYCBP c-myc binding protein
712622	0.000806331 GTF2H2 general transcription factor IIH, polypeptide 2 (44kD subunit)
1573946	7.33E-06 MRPS30 mitochondrial ribosomal protein S30
51700	8.17E-09 ESTs
854444	9.48E-13 HLA-DQB1 major histocompatibility complex, class II, DQ beta 1
712624	0.030232568 Homo sapiens mRNA; cDNA DKFZp564C1216 (from clone DKFZp564C1216)
2054122	6.11E-07 SLC11A3 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3
1698784	0.038568449 Human glucose transporter pseudogene
163579	0.006154605 RAB3A RAB3A, member RAS oncogene family
1641837	0.002757371 Homo sapiens putative ion channel protein CATSPER2 (CATSPER2), mRNA
1472638	0.010481096 FLJ14117 hypothetical protein FLJ14117
1592530	0.010585978 IP6K2 mammalian inositol hexakisphosphate kinase 2
364469	0.007213754 NDUFA7 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (14.5kD, B14.5a)
591157	0.01978301 NET-7 transmembrane 4 superfamily member (tetraspan NET-7)
67070	0.00152487 SLU7 step II splicing factor SLU7
795382	0.000206162 EPAC Rap1 guanine-nucleotide-exchange factor directly activated by cAMP
786562	0.009803386 ZNF43 zinc finger protein 43 (HTF6)
180561	0.001401571 GSTM1 glutathione S-transferase M1
263159	4.66E-06 PL6 PL6 protein
73638	1.57E-05 PTP4A2 protein tyrosine phosphatase type IVA, member 2
156363	0.009457359 FLJ12934 likely ortholog of mouse actin-related protein 8 homolog (S. cerevisiae)
810017-2	0.001130048 PLAUR plasminogen activator, urokinase receptor
1697055	0.022652474 EST

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1031963	1.29E-08 Homo sapiens mRNA; cDNA DKFZp586A0618 (from clone DKFZp586A0618)
306982	0.006503031 ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
1952866	0.004498241 Homo sapiens chromosome 9, P1 clone 11659
46896	1.52E-05 PRO1331 hypothetical protein PRO1331
27516	0.012811838 CAMLG calcium modulating ligand
796330	0.005722733 FLJ14888 hypothetical protein FLJ14888
32050	1.89E-09 Homo sapiens mRNA; cDNA DKFZp586P1124 (from clone DKFZp586P1124)
2017917	0.016701054 Homo sapiens cDNA: FLJ23371 fis, clone HEP16068, highly similar to HSTFIISH Homo sapiens mRNA for transcription elongation factor TFIIIS
823719	0.000166213 ESTs
1585327	0.007304469 AXIN2 axin 2 (conductin, axil)
84068	0.000831262 CL25084 hypothetical protein
1902462	0.048261732 AF038169 hypothetical protein
1733262	1.95E-11 BLu BLu protein
950836	2.86E-08 DDB1 damage-specific DNA binding protein 1 (127kD)
839081	3.95E-05 HELO1 homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2
757435	0.014952072 NKX3A NK homeobox (Drosophila), family 3, A
161993	0.022731389 CEBPB CCAAT/enhancer binding protein (C/EBP), beta
756490	5.64E-05 BCAT2 branched chain aminotransferase 2, mitochondrial
250069	0.001412816 DUSP8 dual specificity phosphatase 8
809939-2	0.000350689 MAPK3 mitogen-activated protein kinase 3
825323	0.004670589 CKAP1 cytoskeleton-associated protein 1
2018581	1.22E-05 IL6ST interleukin 6 signal transducer (gp130, oncostatin M receptor)
788180	0.011295686 AMACR alpha-methylacyl-CoA racemase
741790	0.000210007 FLJ20080 hypothetical protein FLJ20080
193736-2	0.035288396 BRCA2 breast cancer 2, early onset
344168	0.003024674 POLL polymerase (DNA directed), lambda
812227	0.017120553 SLC9A1 solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amiloride sensitive)
741795	6.69E-06 RALGPS1A Ral guanine nucleotide exchange factor RalGPS1A
246194	0.000395219 ESTs

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565379	0.001699546 GRB10 growth factor receptor-bound protein 10
325583	3.88E-05 EST
73659	0.022122876 Homo sapiens, clone IMAGE:3463399, mRNA, partial cds
47853	0.037258896 ALDH4A1 aldehyde dehydrogenase 4 family, member A1
198917	0.001513766 Homo sapiens cDNA FLJ32847 fis, clone TEST12003376
358217	0.027049095 GPC4 glypican 4
450301	0.00677521 MLH3 mutL (E. coli) homolog 3
127243	0.009413465 ESTs
194638	0.011615484 ESTs, Weakly similar to alternatively spliced product using exon 13A [H.sapiens]
726703	4.06E-10 Homo sapiens clone 23736 mRNA sequence
814913	2.00E-07 C11orf15 chromosome 11 open reading frame 15
1569306	0.019052814 FLJ14225 hypothetical protein FLJ14225
112541	5.78E-07 Homo sapiens cDNA FLJ30580 fis, clone BRAWH2006996
108667	0.001139656 SF3A1 splicing factor 3a, subunit 1, 120kD
813973	0.044951328 VPS11 vacuolar protein sorting 11 (yeast homolog)
340974	3.20E-05 Homo sapiens cDNA: FLJ23270 fis, clone COL10309, highly similar to HSU33271 Human normal keratinocyte mRNA
1901824	0.001796004 HSPC207 hypothetical protein
1636251	0.001241866 BAG1 BCL2-associated athanogene
700500	0.000197697 PCTK2 PCTAIRE protein kinase 2
51741	0.000159834 RHO6 GTP-binding protein
789147	0.007583738 ENO2 enolase 2, (gamma, neuronal)
265874	0.030801508 NFIC nuclear factor I/C (CCAAT-binding transcription factor)
769901	0.006350535 CDIPT CDP-diacylglycerol--inositol 3-phosphatidylinositol synthase)
785941	0.00543149 ZNF278 zinc finger protein 278
172721	0.006694279 Homo sapiens cDNA FLJ31795 fis, clone NT2R12008812
1908378	0.002044263 MPP3 membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)
70332	0.036594925 ACP2 acid phosphatase 2, lysosomal
731257	8.33E-05 UNC13 UNC13 (C. elegans)-like
825350	0.034288184 KIAA1040 KIAA1040 protein
841393	0.003180363 PRO0149 PRO0149 protein
360518	0.019741126 NGGT1 guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1

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784212	4.52E-09 FLJ20152 hypothetical protein
49481	1.04E-06 FLJ14800 hypothetical protein FLJ14800
49482	0.000459287 ESTs
767236	0.008346481 CGI-51 CGI-51 protein
1570663	1.29E-05 FKBP4 FK506-binding protein 4 (59kD)
1871127	0.005023894 ESTs
745314	0.008936352 HIRIP5 HIRA-interacting protein 5
611373	0.043542397 PROSC proline synthetase co-transcribed (bacterial homolog)
744374	0.032359098 DKFZP564D166 putative ankyrin-repeat containing protein
23282	0.027026711 IK IK cytokine, down-regulator of HLA II
1738537	0.027971153 ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]
1605539	4.91E-07 IDUA iduronidase, alpha-L-
416374	0.007441554 NET-6 tetraspan NET-6 protein
884599	3.77E-06 FLJ10579 hypothetical protein FLJ10579
687990	0.026614804 ARHGEF6 Rac/Cdc42 guanine exchange factor (GEF) 6
2013685	0.025604814 PTDSS2 phosphatidylserine synthase 2
502988	1.97E-05 ZNF20 zinc finger protein 20 (KOX 13)
51774	0.005356389 ESTs
277266	0.000518693 ESTs, Highly similar to T46303 hypothetical protein DKFZp434N1710.1 [H.sapiens]
138788	0.000130376 PRLR prolactin receptor
265103	0.000987968 MMEL2 membrane metallo-endopeptidase-like 2
489657	0.001447974 WRB tryptophan rich basic protein
34795	0.003683559 DAZAP2 DAZ associated protein 2
183170	0.003453647 Homo sapiens cDNA: FLJ23199 fis, clone REC01091
511012	1.21E-07 AGPS alkylglycerone phosphate synthase
814951	0.023784403 Homo sapiens, RIKEN cDNA 2310005G07 gene, clone MGC:10049 IMAGE:3890955, mRNA, complete cds
788518	0.026818494 PXMP3 peroxisomal membrane protein 3 (35kD, Zellweger syndrome)
360539	0.014513254 PPP3CB protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta)
795738	0.013722183 GNG10 guanine nucleotide binding protein 10
810671	1.19E-06 FLJ22269 hypothetical protein FLJ22269
589232	8.03E-05 FLJ11506 hypothetical protein FLJ11506

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309591	0.049912405 EP300 E1A binding protein p300
198960	2.65E-05 LOC51604 CGI-06 protein
713647	0.040280641 TSPAN-3 tetraspan 3
2273013	0.001241866 TESK2 testis-specific kinase 2
1554646	0.034592388 CPT1A carnitine palmitoyltransferase 1, liver
1609836	0.000260109 GLUL glutamate-ammonia ligase (glutamine synthase)
79592	7.09E-05 AKR7A2 aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)
745339	1.79E-05 KIAA0419 KIAA0419 gene product
1499864	0.009095192 ESTs
76252	0.000627204 HSPC134 HSPC134 protein
840768	0.007517578 ATP6L ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD
1916575	0.011828437 BIK BCL2-interacting killer (apoptosis-inducing)
1582050	0.000266243 IMPDH2 IMP (inosine monophosphate) dehydrogenase 2
730633	0.019761169 OA48-18 acid-inducible phosphoprotein
2011308	0.030221619 DKFZP564O0463 DKFZP564O0463 protein
278222	0.010334304 Homo sapiens, clone MGC:10083 IMAGE:3897118, mRNA, complete cds
1559596	1.29E-05 ESTs, Highly similar to AF175283 1 zinc metalloendopeptidase [H.sapiens]
767268	2.03E-06 DPP7 dipeptidylpeptidase 7
1556259	4.63E-09 ALAD aminolevulinate, delta-, dehydratase
1635649	0.000560777 CDS2 CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 2
772888	0.011513725 KIAA1012 KIAA1012 protein
1551317	0.045171023 EST
203350	0.01354434 KIAA0561 KIAA0561 protein
814971	0.001470365 Homo sapiens cDNA FLJ10046 fis, clone HEMBA1001133
859761	0.000282387 PVRL2 poliovirus receptor-related 2 (herpesvirus entry mediator B)
1584746	0.00604339 FLJ22283 hypothetical protein FLJ22283
162211	1.71E-05 ABCD3 ATP-binding cassette, sub-family D (ALD), member 3
1733625	0.023369612 ESTs
279970	0.038137895 ADORA2A adenosine A2a receptor
685626	0.007916953 ATP2B1 ATPase, Ca++ transporting, plasma membrane 1
625458	6.02E-05 MGC3234 hypothetical protein MGC3234
855487	4.99E-06 ASAH N-acylsphingosine amidohydrolase (acid ceramidase)

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1900149	0.000390804 SBB103 hypothetical SBB103 protein
1470333	2.37E-05 APBB2 amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)
192306	8.94E-05 MPP2 membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)
86035	1.21E-05 LOC51015 CGI-111 protein
1573251	2.47E-05 ZAP128 peroxisomal long-chain acyl-coA thioesterase
2021882	0.000110404 SCNN1D sodium channel, nonvoltage-gated 1, delta
376214	6.82E-06 MRPL43 mitochondrial ribosomal protein L43
74677	4.70E-06 Homo sapiens, Similar to RIKEN cDNA A430107J06 gene, clone MGC:21416 IMAGE:4452699, mRNA, complete cds
726779	0.021235222 CNN1 calponin 1, basic, smooth muscle
1870512	0.000932203 TNFRSF14 tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)
1504268	0.002697689 ESTs, Highly similar to dJ25J6.2 [H.sapiens]
43933	0.007274143 MAOA monoamine oxidase A
1941742	0.015997677 GSA7 ubiquitin activating enzyme E1-like protein
700571	0.02055268 CDC14A CDC14 (cell division cycle 14, S. cerevisiae) homolog A
745363	0.006742484 ESTs
380898	0.000625106 AWP1 protein associated with PRK1
1895781	0.000806373 ESTs, Highly similar to AC004836.1 similar to cadherin and Drosophila Fat protein [H.sapiens]
2018958	0.015480089 Homo sapiens cDNA FLJ31025 fis, clone HLUNG2000501
505575	0.000134468 FLJ10116 hypothetical protein FLJ10116
647397	2.31E-09 MAPT microtubule-associated protein tau
149539	0.007870589 MKP-7 MAPK phosphatase-7
47142	0.000743442 PEX12 peroxisomal biogenesis factor 12
838807	0.019798041 MGC11308 hypothetical protein MGC11308
1492276	1.60E-06 EST
240680	6.30E-05 BIG1 brefeldin A-inhibited guanine nucleotide-exchange protein 1
2314197	0.006926366 FLJ12671 hypothetical protein FLJ12671
487301	5.30E-08 FBXL5 f-box and leucine-rich repeat protein 5
360778-2	1.36E-11 ATM ataxia telangiectasia mutated (includes complementation groups A, C and D)
364865	1.95E-05 FLJ21062 hypothetical protein FLJ21062
813261	0.021270804 Homo sapiens clone 23645 mRNA sequence
814209	0.000165303 ESTs

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1883630	2.71E-11 KIAA1547 KIAA1547 protein
324225	1.89E-05 RARRES3 retinoic acid receptor responder (tazarotene induced) 3
229596	0.001770222 TIC SEC7 homolog
1694113	0.030227648 FLJ21031 hypothetical protein FLJ21031
1635681	3.06E-05 NDUFA2 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)
782688	4.97E-07 P28 dynein, axonemal, light intermediate polypeptide
143661	1.59E-05 NTN4 netrin 4
825715	0.019909138 IFI41 interferon-induced protein 41, 30kD
271721	0.011868489 EST
30850	0.001756144 MMP17 matrix metalloproteinase 17 (membrane-inserted)
814214	0.001725113 D8S2298E reproduction 8
796739	1.69E-06 MGC10924 hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5
486374	0.00241838 MGC4645 hypothetical protein MGC4645
855800	0.000428278 PREP prollyl endopeptidase
120006	0.000302823 ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
490251	0.014632388 PPP1R2 protein phosphatase 1, regulatory (inhibitor) subunit 2
270786	1.17E-05 Homo sapiens cDNA FLJ30436 fis, clone BRACE2009037
813279	4.41E-05 APEH N-acylaminoacyl-peptide hydrolase
160656	3.25E-08 LU Lutheran blood group (Auburger b antigen included)
1850224	0.000270348 ESTs
788580	0.008853088 CCNDBP1 cyclin D-type binding-protein 1
82871	0.014746648 SHBG sex hormone-binding globulin
813281	5.45E-13 WWP1 WW domain-containing protein 1
547058	0.014177292 CCNG1 cyclin G1
1416092	0.016682884 CHDH choline dehydrogenase
854874	0.000592334 KIAA0212 KIAA0212 gene product
1631701	0.000187841 JFC1 NADPH oxidase-related, C2 domain-containing protein
854879	0.001309802 SPHK2 sphingosine kinase type 2 isoform
752903	1.78E-08 KIAA0303 KIAA0303 protein
45578	1.91E-05 MAP2K6 mitogen-activated protein kinase kinase 6
51056	0.010636427 CNIL cornichon-like
43977	0.014632388 KIAA0182 KIAA0182 protein

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301380	0.002812591 UGTREL7 UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter
814232	0.043182465 C21orf59 chromosome 21 open reading frame 59
796754	0.00150122 DREV1 CGI-81 protein
824792	0.001312689 BM045 uncharacterized bone marrow protein BM045
814234	3.88E-05 SUCLG2 succinate-CoA ligase, GDP-forming, beta subunit
1915982	0.00065014 Homo sapiens cDNA FLJ32488 fis, clone SKNSH1000086
229901	0.049474849 CTSO cathepsin O
503214	9.28E-09 KIAA1243 KIAA1243 protein
796757	0.037697334 AP3S1 adaptor-related protein complex 3, sigma 1 subunit
1917588	0.048777689 DNASE2 deoxyribonuclease II, lysosomal
271748	6.83E-06 RBMS1 RNA binding motif, single stranded interacting protein 1
49860	9.02E-05 PDK2 pyruvate dehydrogenase kinase, isoenzyme 2
504959	7.12E-10 Homo sapiens mRNA; cDNA DKFZp586G0321 (from clone DKFZp586G0321)
1602284	1.87E-07 EST
687289	0.004049154 Homo sapiens, clone MGC:3245 IMAGE:3505639, mRNA, complete cds
150118	0.017865847 DKFZp434F054 hypothetical protein DKFZp434F054
140354	0.013770597 Homo sapiens, Similar to secretory carrier membrane protein 4, clone MGC:19661 IMAGE:3161979, mRNA, complete cds
786202	0.002899676 Homo sapiens cDNA FLJ13553 fis, clone PLACE1007454
361565	6.41E-05 GLUD1 glutamate dehydrogenase 1
512045	0.042758148 JM1 JM1 protein
591597	0.011216747 TNNT3 troponin I, cardiac
1574252	0.03289313 DKFZP586D0623 DKFZP586D0623 protein
740476	0.002102096 IRF1 interferon regulatory factor 1
951125	1.70E-05 PECO peroxisomal D3,D2-enoyl-CoA isomerase
1636669	0.001613372 FLJ21939 hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2
283124	4.09E-07 Homo sapiens, clone IMAGE:3917549, mRNA, partial cds
79960	0.006425318 RRP40 exosome component Rrp40
25274	2.51E-09 LOC51161 g20 protein
261204	2.66E-16 ESTs, Highly similar to JC5931 high mobility group I HMGI chromosomal protein isoform C-alpha [H.sapiens]
949938	2.51E-07 CST3 cystatin C (amyloid angiopathy and cerebral hemorrhage)

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49883	0.016175391	SYT13 synaptotagmin XIII
155072	8.66E-16	ESTs
502297	0.000223246	POLI polymerase (DNA directed) iota
150137	0.040830931	DKFZP564O123 DKFZP564O123 protein
85450	8.06E-09	ACOX2 acyl-Coenzyme A oxidase 2, branched chain
212542	0.000127809	Homo sapiens mRNA; cDNA DKFZp586J2118 (from clone DKFZp586J2118)
813603	5.67E-06	KIAA1075 KIAA1075 protein
361587	4.46E-05	KIAA1789 KIAA1789 protein
742094	0.003398986	FLJ20950 hypothetical protein FLJ20950
156023	0.019869669	MGC3123 hypothetical protein MGC3123
1558233	8.16E-12	ESTs
229937	5.99E-05	DDX30 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 30
1469084	0.019869669	KIAA0804 KIAA0804 protein
362532	0.002943504	C12orf22 chromosome 12 open reading frame 22
51093	0.003245464	ZNFN2A1 zinc finger protein, subfamily 2A (FYVE domain containing), 1
1631746	5.44E-05	POLM polymerase (DNA directed), mu
51097	1.98E-05	BAIAP3 BAI1-associated protein 3
2108048	8.16E-07	DNB5 DNB5
342181-2	8.94E-21	BCL2 B-cell CLL/lymphoma 2
785293	3.42E-07	HREV107 similar to rat HREV107
1741884	0.001594038	ESTs, Highly similar to IRX3_HUMAN IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-3 [H.sapiens]
48167	0.001837947	FLJ10483 hypothetical protein FLJ10483
155094	0.010881395	DNAJB12 DnaJ (Hsp40) homolog, subfamily B, member 12
842762	0.014914359	FLJ20363 hypothetical protein FLJ20363
1685363	0.003881514	GLRB glycine receptor, beta
1840803	0.032260939	FLJ20686 hypothetical protein FLJ20686
825785	1.01E-05	KIAA0435 KIAA0435 gene product
2016644	0.009775018	LIMD1 LIM domains containing 1
255754	2.24E-06	LOC51297 LUNX protein; PLUNC (palate lung and nasal epithelium clone); tracheal epithelium enriched protein
159380	0.000970624	FLJ23462 duodenal cytochrome b
159381	1.10E-06	RARA retinoic acid receptor, alpha

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1517749	0.012504399 ESTs	
712314	3.40E-05 MIR myosin regulatory light chain interacting protein	
2284924	1.10E-14 KIAA0882 KIAA0882 protein	
1475662	0.00802641 AXUD1 AXIN1 up-regulated	
1637647	7.42E-05 ESTs	
878744	0.012204566 TSG101 tumor susceptibility gene 101	
824052	0.031302263 C6orf1 chromosome 6 open reading frame 1	
40695	0.044959539 NABP N-ethylmaleimide-sensitive factor attachment protein, beta	
773152	0.001310908 ESTs	
289057	0.004505214 HT021 HT021	
120271-2	0.015988127 MGC4692 hypothetical protein MGC4692	
744010	7.00E-05 Homo sapiens mRNA; cDNA DKFZp586K1318 (from clone DKFZp586K1318)	
79216	0.008448199 AHNAK AHNAK nucleoprotein (desmoyokin)	
842785	0.011581406 LRPAP1 low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1)	
41647	1.11E-06 PTPRT protein tyrosine phosphatase, receptor type, T	
549016	0.019299231 BTBD1 BTB (POZ) domain containing 1	
705110	0.001790158 CASP9 caspase 9, apoptosis-related cysteine protease	
2313921	0.001677464 NDUFB3 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (12kD, B12)	
810305	0.002373538 Homo sapiens cDNA FLJ30463 fis, clone BRACE2009517	
289060	0.000990298 HSPA4 heat shock 70kD protein 4	
262996	0.02908529 CHD1 chromodomain helicase DNA binding protein 1	
687638	0.006365847 ESTs	
1670688	0.006338445 BACH2 BTB and CNC homology 1, basic leucine zipper transcription factor 2	
154466	5.44E-05 STUB1 STIP1 homology and U-Box containing protein 1	
52071	0.026442939 ESTs, Highly similar to AC004836 1 similar to cadherin and Drosophila Fat protein [H.sapiens]	
301740	0.018221151 Homo sapiens cDNA FLJ30298 fis, clone BRACE2003172	
52076	0.000531118 OLFM1 olfactomedin 1	
34439	0.000548494 FUS2 putative tumor suppressor	
428184	8.50E-10 Homo sapiens, clone MGC:18216 IMAGE:4156235, mRNA, complete cds	
743081	0.048000809 NDUFA3 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3 (9kD, B9)	
565062	0.023268805 Homo sapiens clone 24812 mRNA sequence	

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31893	0.010529568 LOC84548 hypothetical protein from Xq28
646057	0.010403382 Homo sapiens cDNA: FLJ21897 fis, clone HEP03447, highly similar to AF052178 Homo sapiens clone 24523 mRNA sequence
809779	8.13E-08 KIAA0239 KIAA0239 protein
1575263	0.005751783 DKFZP586N0721 DKFZP586N0721 protein
773170	2.17E-06 TPBG trophoblast glycoprotein
853506	0.002203842 PISD phosphatidylserine decarboxylase
757135	2.60E-05 DKFZP564J0123 DKFZP564J0123 protein
381166	3.78E-06 MORF histone acetyltransferase
361922	0.040228151 ZMPSTE24 zinc metalloproteinase, STE24 (yeast, homolog)
50484	2.41E-05 CCRK cell cycle related kinase
281590	0.026213959 FLJ10656 hypothetical protein FLJ10656
1700621	0.001782567 EGFL4 EGF-like-domain, multiple 4
26289	0.041064782 FLJ12879 hypothetical protein FLJ12879
565075	0.000170815 STC1 stanniocalcin 1
1568056	0.005442251 ESTs, Moderately similar to I78885 serine/threonine-specific protein kinase [H.sapiens]
252453	0.00590112 LOC51635 CGI-86 protein
810325	2.48E-05 IVD isovaleryl Coenzyme A dehydrogenase
1469425	0.00010497 SOX22 SRY (sex determining region Y)-box 22
781342	2.74E-05 MGC11115 hypothetical protein MGC11115
154482	1.29E-05 SERPINB1 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1
845352	0.000586706 NUDT9 nudix (nucleoside diphosphate linked moiety X)-type motif 9
266500	2.03E-08 ESTs
773185	0.008673574 ESTs
136845	0.024067407 Homo sapiens, clone IMAGE:3915000, mRNA
1870938	0.007988734 CDS1 CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 1
310584	7.42E-05 ARL1 ADP-ribosylation factor-like 1
1585040	1.45E-08 TCEB1L transcription elongation factor B (SIII), polypeptide 1-like
1916225	0.005767924 ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]
26294	2.07E-09 RNB6 RNB6
416042	0.000488136 Homo sapiens cDNA FLJ31053 fis, clone HSYRA2000640, highly similar to Homo sapiens FRG1 mRNA
248583	0.036283521 NFX1 nuclear transcription factor, X-box binding 1

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344959	2.38E-09 HSA250839 gene for serine/threonine protein kinase
2010012	0.004201172 P37NB 37 kDa leucine-rich repeat (LRR) protein
71763	0.001262603 SIP Siah-interacting protein
154493	0.015871 IFI41 interferon-induced protein 41, 30kD
2054945	0.000649145 SLC23A2 solute carrier family 23 (nucleobase transporters), member 2
797000	0.011811432 TERE1 transitional epithelia response protein
594517	0.036288061 SFRS6 splicing factor, arginine/serine-rich 6
206341	0.011625517 ESTs, Weakly similar to A49364 59 protein, brain [H.sapiens]
280950	4.51E-05 SRI sorcin
109316	0.006324487 SERPINA3 serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3
203003	0.002285045 NME4 non-metastatic cells 4, protein expressed in
503602	0.000403283 PRO1489 hypothetical protein PRO1489
769600	0.013770597 UNG2 uracil-DNA glycosylase 2
1968246	1.12E-05 FUT8 fucosyltransferase 8 (alpha (1,6) fucosyltransferase)
432093	2.37E-06 IL18BP interleukin 18 binding protein
1879094	0.002741302 FLJ23392 hypothetical protein FLJ23392
782306	3.08E-06 FLJ13110 hypothetical protein FLJ13110
1635307	4.84E-05 Homo sapiens, clone IMAGE:3833472, mRNA
1420370	0.036288061 BLVRB biliverdin reductase B (flavin reductase (NADPH))
284160	3.04E-08 CACNA2D2 calcium channel, voltage-dependent, alpha 2/delta subunit 2
595181	0.000601881 MIR myosin regulatory light chain interacting protein
470348	0.001309802 ESTs
1926007	0.00216623 EST
33817	7.74E-06 ESTs
1456348	0.020321818 SAS N-acetylneuraminic acid phosphate synthase; sialic acid synthase
1056172	0.002436429 NMES1 normal mucosa of esophagus specific 1
84880	0.000162089 LOC51004 CGI-10 protein
491612	0.000816756 Homo sapiens cDNA FLJ11752 fis, clone HEMBA1005582, weakly similar to TROPOMYOSIN 1, NON-MUSCLE ISOFORM
344970	0.009457359 ITGA4 integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)
796079	0.001202428 MGC4171 hypothetical protein MGC4171

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504279	0.016946636 TBL1 transducin (beta)-like 1
898333	0.04010901 ESTs
950574	0.013952573 H3F3B H3 histone, family 3B (H3.3B)
250883	0.010544493 UBE1L ubiquitin-activating enzyme E1-like
230560	0.003417271 ESTs
666707	0.002506551 ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
825060	0.012784217 DUT dUTP pyrophosphatase
1690262	0.032703827 Homo sapiens cDNA FLJ20763 fis, clone COL09911
788208	7.66E-07 FLJ10659 hypothetical protein FLJ10659
265592	0.019761169 Homo sapiens, activated RNA polymerase II transcription cofactor 4, clone MGC:21503 IMAGE:3881373, mRNA, complete cds
291399	0.000155359 HMG2 high-mobility group (nonhistone chromosomal) protein 2
262251	0.000333214 CLCN7 chloride channel 7
786607	0.000772083 TCEAL1 transcription elongation factor A (SII)-like 1
108395	1.56E-05 DLG5 discs, large (Drosophila) homolog 5
245273	0.019521612 LOC57020 hypothetical protein
626861	0.009420842 EIF4G2 eukaryotic translation initiation factor 4 gamma, 2
1323361	0.008588081 NR2F6 nuclear receptor subfamily 2, group F, member 6
489351	0.00010205 DKFZP566J2046 hypothetical protein DKFZp566J2046
2054977	0.000148287 KIAA0373 KIAA0373 gene product
26617	0.000316752 ALCAM activated leucocyte cell adhesion molecule
268148	0.000875061 TRIM4 tripartite motif-containing 4
665774	0.049423242 EIF4E eukaryotic translation initiation factor 4E
797038	0.011982092 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1502032
1652310	0.017604138 Homo sapiens cDNA FLJ30306 fis, clone BRACE2003319
562867	0.044978437 RRS1 homolog of yeast ribosome biogenesis regulatory protein RRS1
1880743	0.008335378 ESTs
38781	0.03544066 ATP9B ATPase, Class II, type 9B
1609538	3.46E-05 KIAA1324 KIAA1324 protein
487761	0.034130662 TAF2S TATA box binding protein (TBP)-associated factor, RNA polymerase II, S, 150kD
36491-2	0.00247482 ESTs
755599	0.023780533 IFITM1 interferon induced transmembrane protein 1 (9-27)

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2017684	0.000107787 LOC51644 CGI-120 protein
244637	0.000498127 CRI1 CREBBP/EP300 inhibitory protein 1
156437-2	0.001309095 ATP1A2 ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide
2222453	0.028657358 EHD2 EH-domain containing 2
53092	0.008880977 KIAA0436 putative L-type neutral amino acid transporter
841415	4.94E-05 EPLIN epithelial protein lost in neoplasm beta
770983	0.010403382 FLJ11730 hypothetical protein FLJ11730
363590	0.00042623 ARNT2 aryl hydrocarbon receptor nuclear translocator 2
1586043	0.018119429 ESTs
2709505	4.45E-08 LPHB lipophilin B (uteroglobin family member), prostatein-like
204790	2.03E-09 FLJ20273 hypothetical protein
1897065	0.017531828 SMUG1 single-strand selective monofunctional uracil DNA glycosylase
487777	0.02848343 RB1 retinoblastoma 1 (including osteosarcoma)
263229	0.001149746 LAF4 lymphoid nuclear protein related to AF4
1911343	3.74E-12 RAB26 RAB26, member RAS oncogene family
1558642	1.95E-11 MLPH melanophilin
60602	3.22E-06 CSH1 chorionic somatomammotropin hormone 1 (placental lactogen)
156437	0.036072406 ATP1A2 ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide
730346	0.003570072 HEBP1 heme binding protein 1
143332	0.005649342 NPY1R neuropeptide Y receptor Y1
32122	2.31E-09 FLJ10210 hypothetical protein FLJ10210
195346	7.13E-06 FLJ00005 FLJ00005 protein
786640	0.005990788 VEZATIN transmembrane protein vezatin
109379	0.003007609 HMGCR 3-hydroxy-3-methylglutaryl-Coenzyme A reductase
590298	0.023157899 MRPL45 mitochondrial ribosomal protein L45
645485	0.005375632 TERF1 telomeric repeat binding factor (NIMA-interacting) 1
134523	5.65E-05 EMAP-2 microtubule-associated protein like echinoderm EMAP
134525	0.013501077 CUL3 cullin 3
44292	0.027304029 Homo sapiens mRNA; cDNA DKFZp434C107 (from clone DKFZp434C107)
140008	0.018500323 EBNA1BP2 EBNA1-binding protein 2
511831	3.46E-05 MGC12936 hypothetical protein MGC12936
2014373	0.0330879 HNK-1ST HNK-1 sulfotransferase

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928315	0.014172516	CARKL carbohydrate kinase-like
172495	0.002069329	KIAA0028 leucyl-tRNA synthetase, mitochondrial
724888	4.45E-05	CYP4B1 cytochrome P450, subfamily IVB, polypeptide 1
296679	0.0002926	Homo sapiens clone TCCTA00151 mRNA sequence
357344	0.035245897	KCNQ1 potassium voltage-gated channel, KQT-like subfamily, member 1
843046	0.009533011	GPRK7 G protein-coupled receptor kinase 7
789204	0.001843366	TLOC1 translocation protein 1
183200	0.012787936	FAH fumarylacetoacetate hydrolase (fumarylacetoacetase)
744417	0.006558294	CRAT carnitine acetyltransferase
812300	0.003557075	FLJ20265 hypothetical protein FLJ20265
418019	0.001030569	KIAA0542 KIAA0542 gene product
1569096	0.022893459	ESTs
79629-2	0.014086588	CXCR4 chemokine (C-X-C motif), receptor 4 (fusin)
782385	0.031219133	DKFZP566D193 DKFZP566D193 protein
897745	0.002311826	FLJ13868 hypothetical protein FLJ13868
843054	0.004353571	KIAA1533 KIAA1533 protein
826070	0.017970183	ZFP91 zinc finger protein homologous to Zfp91 in mouse
1608928	0.028565804	CYP4F11 cytochrome P450, subfamily IVF, polypeptide 11
564801	0.006100942	Homo sapiens cDNA: FLJ21409 fis, clone COL03924
826077	0.000373482	PDHB pyruvate dehydrogenase (lipoamide) beta
177737	0.014789221	PURA purine-rich element binding protein A
823819	0.001641999	EST
83508	0.026147968	B9 B9 protein
795498	0.001139656	HS1-2 putative transmembrane protein
505299	0.000389422	BBP beta-amyloid binding protein precursor
49546	0.02081588	P29 GCIP-interacting protein p29
2028440	0.001074094	ESTs
346942	0.0003267	PIGQ phosphatidylinositol glycan, class Q
34849	0.017962259	EEF2 eukaryotic translation elongation factor 2
247230	0.011626312	Homo sapiens cDNA FLJ30532 fis, clone BRAWH2001129, weakly similar to OCCLUDIN
50888	0.000228763	PRDX3 peroxiredoxin 3
754998	0.039096645	SRP19 signal recognition particle 19kD

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2168667	0.002032038 POLR2H polymerase (RNA) II (DNA directed) polypeptide H
724112	0.001610749 ESTs, Weakly similar to B34087 hypothetical protein [H.sapiens]
741891	2.17E-05 RAB2L RAB2, member RAS oncogene family-like
130276	0.027971153 Homo sapiens mRNA; cDNA DKFZp586H0324 (from clone DKFZp586H0324)
66535	0.000646325 OAZ2 ornithine decarboxylase antizyme 2
1500000	0.000577003 H2BFB H2B histone family, member B
1049330	0.000116235 SSPN sarcospan (Kras oncogene-associated gene)
1683411	0.000739744 ESTs
611443	0.000106149 MB myoglobin
591281	0.021583844 MVP major vault protein
504657	0.013710873 KIAA0438 KIAA0438 gene product
810734	6.48E-09 POLD4 polymerase (DNA-directed), delta 4
2297394	0.022064191 FLJ13612 hypothetical protein FLJ13612
1901924	0.014853485 ESTs, Weakly similar to T21364 hypothetical protein F25H5.6 - Caenorhabditis elegans [C.elegans]
1553766	0.000795582 FLJ10283 hypothetical protein FLJ10283
267571	2.41E-06 SNAPC2 small nuclear RNA activating complex, polypeptide 2, 45kD
1588791	0.02123298 MGMT O-6-methylguanine-DNA methyltransferase
1049346	1.26E-05 FOXP1 forkhead box P1
121470	0.030626 BCCIP BRCA2 and CDKN1A-interacting protein
298603	0.005015434 KIAA1474 KIAA1474 protein
1569418	2.89E-07 Homo sapiens cDNA FLJ11385 fis, clone HEMBA1000520
782700	0.000804231 CLASP2 CLIP-associated protein 2
884677	3.02E-05 Homo sapiens, clone IMAGE:3611719, mRNA, partial cds
782702	8.52E-08 LOC56270 hypothetical protein 628
108425-2	0.006209446 ESTs, Weakly similar to JC5314 CDC28/cdc2-like kinase associating arginine-serine cyclophilin [H.sapiens]
154103	0.000352444 SCN1B sodium channel, voltage-gated, type I, beta polypeptide
759163	2.95E-13 MFAP4 microfibrillar-associated protein 4
1566877	0.020116819 C11orf2 chromosome 11 open reading frame2
1635705	0.016769168 ESTs, Highly similar to T46422 hypothetical protein DKFZp434M2023.1 [H.sapiens]
35812	0.022973459 PCLO piccolo (presynaptic cytomatrix protein)
51851	0.004091636 ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]

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1839935	2.36E-06 ESTs
2169632	0.022764168 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 42138
669359	0.00497373 Homo sapiens clone 24405 mRNA sequence
1625945	0.004424523 NDRG3 N-myc downstream-regulated gene 3
682058	0.00167005 SPOP speckle-type POZ protein
752625	0.00014539 Homo sapiens mRNA; cDNA DKFZp667D095 (from clone DKFZp667D095)
843094	0.046423899 UBL1 ubiquitin-like 1 (sentrin)
298610	0.007478622 Homo sapiens cDNA FLJ13927 fis, clone Y79AA1000627, moderately similar to Homo sapiens zinc finger protein (ZF5128) mRNA
299274	0.033282881 Homo sapiens cDNA FLJ32430 fis, clone SKMUS2001129, weakly similar to NAD-DEPENDENT METHANOL DEHYDROGENASE (EC 1.1.1.244)
41302	0.002068339 KIAA0643 KIAA0643 protein
682063	0.001692383 ZNF189 zinc finger protein 189
824802	1.92E-05 HTGN29 HTGN29 protein
35828	0.024474794 DTR diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)
283919	0.046763683 H2AFL H2A histone family, member L
868652	4.71E-08 C4B complement component 4B
1668067	7.31E-05 DKFZP434D146 DKFZP434D146 protein
345247	0.007295582 ESTs, Moderately similar to T03094 A-kinase anchor protein DAKAP550 - fruit fly [D.melanogaster]
823867	0.005767924 ESTs
2455403	0.000513257 ZNF91 zinc finger protein 91 (HPF7, HTF10)
366511	0.003874401 ACTA1 actin, alpha 1, skeletal muscle
767346	0.017970183 C14orf4 chromosome 14 open reading frame 4
241474-2	0.000122034 BRCA1 breast cancer 1, early onset
772962	0.00014351 Homo sapiens cDNA FLJ31149 fis, clone IMR322001491, moderately similar to Rattus norvegicus tricarboxylate carrier-like protein mRNA
855559	2.45E-10 SAS sarcoma amplified sequence
36491	0.01049982 ESTs
669379	0.031219133 Homo sapiens, clone IMAGE:3463399, mRNA, partial cds
36493	0.015997677 NAGA N-acetylgalactosaminidase, alpha-
282980	0.001343272 ESTs
752643	1.91E-05 PLA2G12 group XII secreted phospholipase A2

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69124	0.000606588 CIRBP cold inducible RNA-binding protein
566466	0.01931096 HSU93850 elongation factor-2 kinase
510170	0.000277083 PAIP2 PABP-interacting protein 2
855563	5.61E-05 ERBB3 v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3
139835	7.14E-08 UGDH UDP-glucose dehydrogenase
154138	0.024566797 Homo sapiens cDNA FLJ32174 fis, clone PLACE6001064
2284619	0.011581406 ZNF132 zinc finger protein 132 (clone pHZ-12)
460218	0.018807962 EST
488025	0.000960715 ZNF226 zinc finger protein 226
745437	0.003016551 ESTs
208387	0.000636782 KIAA1407 KIAA1407 protein
1843843	0.025604134 SRGAP1 KIAA1304 protein
258790	0.006397727 CCK cholecystokinin
205049	0.000551716 H11 protein kinase H11
490306	0.000487266 TM9SF1 transmembrane 9 superfamily member 1
773922	0.004876463 BZAP45 basic leucine-zipper protein BZAP45
66599	1.39E-11 NAT1 N-acetyltransferase 1 (arylamine N-acetyltransferase)
280602	0.000362169 ESTs
488033	0.002117729 DNAJB9 DnaJ (Hsp40) homolog, subfamily B, member 9
1860836	0.007295582 Homo sapiens cDNA FLJ30927 fis, clone FEBRA2006736
726860	0.011916108 C11orf14 chromosome 11 open reading frame 14
840878	0.000600849 DHCR24 24-dehydrocholesterol reductase
1702695	0.003491873 MRPL53 mitochondrial ribosomal protein L53
289830	0.024964587 KIAA0329 KIAA0329 gene product
1569465	0.027305675 IGHMBP2 immunoglobulin mu binding protein 2
2367226	0.001193191 HRC histidine-rich calcium-binding protein
2048040	0.002874419 Homo sapiens cDNA FLJ32130 fis, clone PEBLM2000248, weakly similar to ZINC FINGER PROTEIN 157
810791	0.006604078 MINAT1 menage a trois 1 (CAK assembly factor)
810795	1.05E-05 FLJ21940 hypothetical protein FLJ21940
1561981	7.62E-05 EST
28643	5.46E-05 DKFZP564D1378 hypothetical protein DKFZP564D1378

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665405	4.33E-05 MYO5C myosin 5C
1518402	1.68E-09 KIAA1361 KIAA1361 protein
283956	6.52E-05 Homo sapiens cDNA FLJ13155 fis, clone NT2RP3003433
840882	1.48E-06 NBP nucleotide binding protein
742115	1.20E-06 DCI dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
809464	0.015509308 FGFR2 fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)
85195	0.00013313 GADD45G growth arrest and DNA-damage-inducible, gamma
1521341	8.51E-05 HIRIP3 HIRA-interacting protein 3
768324	0.010220908 KIAA0107 KIAA0107 gene product
210688	1.39E-12 ADCY9 adenylate cyclase 9
1557318	0.028091838 ESTs
1636707	0.010283446 EIF3S3 eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD)
837953	1.10E-05 NEDD4L neural precursor cell expressed, developmentally down-regulated 4-like
429906	0.009533011 PIGN phosphatidylinositol glycan, class N
530814	0.000234182 SEPP1 selenoprotein P, plasma, 1
258026	0.000719645 EST
41356	0.035107908 PPP2R5A protein phosphatase 2, regulatory subunit B (B56), alpha isoform
1631487	0.001988084 ESTs
752688	1.73E-05 ESTs
565849	0.000900648 C3IP1 kelch-like protein C3IP1
1699142	3.36E-05 AP1G2 adaptor-related protein complex 1, gamma 2 subunit
253884	0.043335326 Homo sapiens, clone IMAGE:3625286, mRNA, partial cds
810017	0.000594167 PLAUR plasminogen activator, urokinase receptor
1422723	0.02727988 IFI35 interferon-induced protein 35
1868349	0.023383495 PLA2G4B phospholipase A2, group IVB (cytosolic)
730768	9.62E-05 Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245)
1537001	0.012963093 ESTs
470261-2	0.000165604 SMA5 SMA5
712049	0.01747597 IL24 interleukin 24
526945	0.013261832 FABGL FabG (beta-ketoacyl-[acyl-carrier-protein] reductase, E coli) like
814306	0.020168182 TPD52 tumor protein D52

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726890	0.00099919 MGC4643 hypothetical protein MGC4643
1572710	0.00888435 FLJ21213 hypothetical protein FLJ21213
809488	0.007951698 RAI17 retinoic acid induced 17
502349	2.77E-06 CAB56184 hypothetical protein CAB56184
781046	0.000438842 ERBB2IP erbb2-interacting protein ERBIN
782787	2.14E-05 FLJ21347 hypothetical protein FLJ21347
365919	6.59E-07 STAU stauflen (Drosophila, RNA-binding protein)
1898442	0.001557478 ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]
1908840	1.16E-05 ZNF174 zinc finger protein 174
2298710	0.012030871 TRIM16 tripartite motif-containing 16
1560279	0.02187025 Homo sapiens clone CDABP0155 mRNA sequence
743880	0.014144736 KIAA0263 KIAA0263 gene product
824879	5.97E-08 MGC11275 hypothetical protein MGC11275
270883	0.001399452 GNIM3 cyclin M3
341316	2.88E-07 HTATSF1 HIV TAT specific factor 1
1910040	2.37E-06 LOC51701 nemo-like kinase
81229	0.00100873 FTL ferritin, light polypeptide
811774	5.01E-08 LOC51097 CGI-49 protein
1521375	8.48E-06 Homo sapiens cDNA FLJ13542 fis, clone PLACE1006779
839583	0.01394813 ESTs, Moderately similar to T46386 hypothetical protein DKFZp434P011.1 [H.sapiens]
214205	9.59E-12 Homo sapiens, clone MGC:17687 IMAGE:3865868, mRNA, complete cds
825822	0.000681333 DJ167A19.1 hypothetical protein
1762111	0.000300738 NPR3 natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)
487425	0.001309802 CETN3 centrin, EF-hand protein, 3 (CDC31 yeast homolog)
195786	0.000395849 EST
2298723	0.014679158 KIAA0708 KIAA0708 protein
66931	0.023818015 FLJ20307 hypothetical protein FLJ20307
490360	0.018119429 MGC5560 hypothetical protein MGC5560
767706	3.86E-05 ESTs
1732033	0.00024242 FLJ14427 hypothetical protein FLJ14427
234537	0.039367559 Homo sapiens, clone IMAGE:3869590, mRNA, partial cds
1631807	0.013415846 GMPPB GDP-mannose pyrophosphorylase B

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2017352	0.003753263 B4GALT7 xylosylprotein beta1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)
361659	0.023660933 DKFZP434D146 DKFZP434D146 protein
66946	0.017962259 U2AF1RS2 U2 small nuclear ribonucleoprotein auxiliary factor, small subunit 2
1610546	2.73E-11 HNF3A hepatocyte nuclear factor 3, alpha
811790	0.024330122 DKFZP564G0222 DKFZP564G0222 protein
951216	0.001063475 NDUFB10 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (22kD, PDSW)
811792	0.00199207 GSS glutathione synthetase
813396	0.006131911 KIAA1204 KIAA1204 protein
242706	0.033985397 HSPC274 HSPC274 protein
173878	0.005539042 MGC14327 hypothetical protein MGC14327
52103	3.48E-05 FLJ23045 hypothetical protein FLJ23045
450810	0.031458387 FLJ12154 hypothetical protein FLJ12154
592630	0.002077599 MINPP1 multiple inositol polyphosphate histidine phosphatase, 1
1156538	4.81E-16 ESTs
487444	0.015004486 ARPP-19 cyclic AMP phosphoprotein, 19 kD
273454	0.016029967 ESTs
2296063	0.010400431 KIAA0528 KIAA0528 gene product
120138	0.000909767 JDP1 J domain containing protein 1
810063	0.016542848 GFER growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)
1635022	0.007124761 DDAH2 dimethylarginine dimethylaminohydrolase 2
144740	6.16E-11 SDCCAG28 serologically defined colon cancer antigen 28
470061	8.03E-07 SIAH2 seven in absentia (Drosophila) homolog 2
1631820	0.038581914 ESTs
1456060	0.004330191 ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]
230271	0.000257296 AD-017 glycosyltransferase AD-017
138189	4.90E-09 WFS1 Wolfram syndrome 1 (wolframin)
842838	0.020243356 TADA3L transcriptional adaptor 3 (ADA3, yeast homolog)-like (PCAF histone acetylase complex)
2028876	7.96E-05 SFRS5 splicing factor, arginine/serine-rich 5
1632487	0.02848343 WISP2 WNT1 inducible signaling pathway protein 2
530875	0.001185188 TKT transketolase (Wernicke-Korsakoff syndrome)
814350	0.010880033 IDE insulin-degrading enzyme
432108	0.001273848 I-1 imidazoline receptor candidate

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814353	0.012831119 PMAIP1 phorbol-12-myristate-13-acetate-induced protein 1
726147	0.024330122 MAP2K4 mitogen-activated protein kinase kinase 4
23776	3.95E-07 QDPR quinoid dihydropteridine reductase
503338	0.000584849 WT1 Wilms tumor 1
156117	0.033291452 Homo sapiens, clone IMAGE:3884331, mRNA, partial cds
768395	0.013459172 ESTs
898058	0.001034397 ESTs
1854648	0.000117862 HPX hemopexin
35147	2.97E-07 ESTs, Weakly similar to UOG1_HUMAN UOG-1 PROTEIN [H.sapiens]
2388571	0.001899953 AKAP8 A kinase (PRKA) anchor protein 8
809828	1.10E-13 E2F5 E2F transcription factor 5, p130-binding
811024	7.03E-05 BST2 bone marrow stromal cell antigen 2
625923	0.015565633 PCK2 phosphoenolpyruvate carboxykinase 2 (mitochondrial)
1882051	0.014745604 FLJ20080 hypothetical protein FLJ20080
121898	2.79E-06 Homo sapiens mRNA; cDNA DKFZp586J0720 (from clone DKFZp586J0720)
1583198	1.28E-06 ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens]
1031727	0.012784217 SIRT2 sirtuin (silent mating type information regulation 2, S.cerevisiae, homolog) 2
810088	0.025874177 FLJ20258 hypothetical protein FLJ20258
241798	0.03154152 Homo sapiens cDNA FLJ30407 fis, clone BRACE2008553
85561	4.23E-05 CYP2A7 cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7
809838	0.032429761 EST
743146	7.92E-05 FLJ23403 hypothetical protein FLJ23403
489079	0.003602021 IL2RB interleukin 2 receptor, beta
361698	0.002131744 LIPE lipase, hormone-sensitive
49204	0.00050472 Homo sapiens mRNA; cDNA DKFZp566A1046 (from clone DKFZp566A1046)
811038	0.016882187 LOC51238 hypothetical protein
2012454	0.045950427 Homo sapiens, clone IMAGE:4391536, mRNA
155197	3.41E-06 ESTs
470092	0.001366354 LARGE like-glycosyltransferase
1412245	0.016770876 CPA2 carboxypeptidase A2 (pancreatic)
488422	0.028019793 HMG20B high-mobility group 20B
1635059	2.23E-09 Homo sapiens, clone MGC:16638 IMAGE:4121964, mRNA, complete cds

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345663	0.002436388 RAMP3 receptor (calcitonin) activity modifying protein 3
42389	0.002362537 ESTs, Weakly similar to Z195_HUMAN ZINC FINGER PROTEIN 195 [H.sapiens]
203846	0.037582255 FLJ22060 hypothetical protein FLJ22060
1894519	0.000251134 FLJ12085 hypothetical protein FLJ12085
74070	0.000230079 ENSA endosulfine alpha
627542	6.23E-06 BLVRA biliverdin reductase A
773240	0.02515722 ALG5 Alg5, S. cerevisiae, homolog of
1562231	0.007588458 SETBP1 SET binding protein 1
1635062	9.01E-06 DKFZP586A011 DKFZP586A011 protein
773248	0.000803586 Homo sapiens cDNA FLJ31373 fis, clone NB9N42000342
898083	0.041184366 HBOA histone acetyltransferase
291426	0.001816883 KIAA1846 similar to acetyl-coenzyme A synthetase
123802	1.92E-06 MFAP1 microfibrillar-associated protein 1
177419	9.51E-05 SH3GLB2 SH3-domain, GRB2-like, endophilin B2
309316	0.040000458 LOC58498 myosin light chain 2a
627555	0.001343272 MGC3020 hypothetical protein MGC3020
1637751	0.001227916 OXA1L oxidase (cytochrome c) assembly 1-like
49229	0.000209018 GPHN gephyrin
781418	0.011924329 NPIP nuclear pore complex interacting protein
767775	0.011293731 LOC51242 hypothetical protein
48285	0.000352444 PIG11 p53-induced protein
785701	0.011615484 RAB31 RAB31, member RAS oncogene family
809869	0.020168182 ESTs
810402	0.002154308 LOC51248 hypothetical protein
785708	0.044838359 ESTs, Weakly similar to O4HUD1 debrisoquine 4-hydroxylase [H.sapiens]
2306804	1.41E-11 PSMD13 proteasome (prosome, macropain) 26S subunit, non-ATPase, 13

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Table 2. Genes that are overexpressed in ER negative cells, and underexpressed in ER positive cells

Clone_ID	P_value	Gene_Description
1557714	0.000249393	ADAM19 a disintegrin and metalloproteinase domain 19 (meltrin beta)
340745	0.000173284	Homo sapiens cDNA FLJ31683 fis, clone NT2R12005353
325365	0.00025078	HRB2 HIV-1 rev binding protein 2
1467905	0.032429761	NSG-X brain and nasopharyngeal carcinoma susceptibility protein
757225	0.002362784	SNX3 sorting nexin 3
140806	0.002900139	PAM peptidylglycine alpha-amidating monooxygenase
796134	0.000177795	MAP3K7 mitogen-activated protein kinase kinase 7
842896	0.018473624	DKFZp762L0311 hypothetical protein DKFZp762L0311
1550894	3.48E-08	ESTs, Highly similar to A46297 beta-1,6-N-acetylglucosaminyltransferase [H.sapiens]
813751	0.028826444	SIAT4C sialyltransferase 4C (beta-galactosidase alpha-2,3-sialyltransferase)
740925	0.012998471	INDO indoleamine-pyrrole 2,3 dioxygenase
795191	1.39E-05	XPNPEP1 X-prolyl aminopeptidase (aminopeptidase P) 1, soluble
824179	0.016037507	KIAA0655 huntingtin interacting protein-1-related
731023	0.020902723	WDR5 WD repeat domain 5
2016775	4.63E-09	GPRC5B G protein-coupled receptor, family C, group 5, member B
324712	0.023557456	RPS6KB2 ribosomal protein S6 kinase, 70kD, polypeptide 2
2326057	0.000136732	MLN51 MLN51 protein
795197	0.000998067	UBE2E2 ubiquitin-conjugating enzyme E2E 2 (homologous to yeast UBC4/5)
1570427	0.000231261	MGC4309 hypothetical protein MGC4309
199367	2.20E-05	TNRC3 trinucleotide repeat containing 3
40021	0.002599711	HR hairless (mouse) homolog
884355	0.000576316	WASF3 WAS protein family, member 3
1257131	2.20E-05	ESTs, Weakly similar to SYN1 MOUSE SYNAPSIN I [M.musculus]
731031	5.77E-06	LOC51622 CGI-43 protein
415191	1.80E-12	KIAA0161 KIAA0161 gene product
1637781	0.00021037	EST
1858992	0.004823705	KIAA0615 KIAA0615 gene product
712454	2.82E-06	Homo sapiens mRNA; cDNA DKFZp434O1317 (from clone DKFZp434O1317)

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1911099	0.02187025 SCYA8 small inducible cytokine subfamily A (Cys-Cys), member 8 (monocyte chemotactic protein 2)
785733	1.41E-05 FLJ12892 hypothetical protein FLJ12892
2009574	0.000167648 T T brachyury (mouse) homolog
490753	0.001096449 FLJ20420 hypothetical protein FLJ20420
502753	0.003728424 ANGPT2 angiotensinogen 2
172517	0.004544404 HPCAL1 hippocampal-like 1
731044	0.006043174 GLRX2 glutaredoxin 2
155532	2.88E-07 ESTs, Highly similar to bK989H11.1 [H.sapiens]
731047	5.13E-08 ESTs
49266	0.001856861 LOC51667 NEDD8 ultimate buster-1
1723604	0.000868338 MSP mosaic serine protease
1637791	0.001388783 MGC5350 hypothetical protein MGC5350
1759290	9.79E-05 FLJ11264 hypothetical protein FLJ11264
221828	0.003359378 ATSV axonal transport of synaptic vesicles
291478	1.72E-06 RUNX3 runt-related transcription factor 3
141495	0.009886773 SULT2B1 sulfotransferase family, cytosolic, 2B, member 1
1534888	1.05E-06 TNFRSF21 tumor necrosis factor receptor superfamily, member 21
784005	0.003109725 CARD12 caspase recruitment domain protein 12
120516	0.004325708 ESTs
812048	5.76E-07 PRNP prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)
563598	1.56E-09 GABRP gamma-aminobutyric acid (GABA) A receptor, pi
759948	3.06E-06 S100B S100 calcium-binding protein, beta (neural)
757265	0.000137487 MGC4399 hypothetical protein MGC4399
1933324	0.017405243 MPZ myelin protein zero (Charcot-Marie-Tooth neuropathy 1B)
2027515	0.000231471 SFN stratifin
1614140	0.018506461 LOC51285 Ris
526297	0.020076393 NTSR1 neurotensin receptor 1 (high affinity)
113300	0.000965053 TRIM14 tripartite motif-containing 14
1587847	0.000486268 MCM6 minichromosome maintenance deficient (mis5, S. pombe) 6
40056	0.000446292 CSPG4 chondroitin sulfate proteoglycan 4 (melanoma-associated)
270505	0.019185378 MMP14 matrix metalloproteinase 14 (membrane-inserted)

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2017754	0.015486907 DGS1 DiGeorge syndrome critical region gene DGS1; likely ortholog of mouse expressed sequence 2 embryonic lethal
1522734	0.039850127 Homo sapiens cDNA FLJ31090 fis, clone IMR321000102
784016	0.000332608 FLJ20624 hypothetical protein FLJ20624
884388	0.017638942 FLJ21103 hypothetical protein FLJ21103
490772	0.000274015 SNRPA1 small nuclear ribonucleoprotein polypeptide A'
810454	1.82E-05 BACE2 beta-site APP-cleaving enzyme 2
490777	0.001468215 EST
49284	2.69E-08 FGF11 fibroblast growth factor 11
1500815	0.003016551 Homo sapiens cDNA: FLJ22130 fis, clone HEP19632
126413	0.013564319 ITIH2 inter-alpha (globulin) inhibitor, H2 polypeptide
1631132	2.58E-05 PHT2 peptide transporter 3
593690	0.000827726 TNFSF13B tumor necrosis factor (ligand) superfamily, member 13b
133637	0.007572041 PRKDC protein kinase, DNA-activated, catalytic polypeptide
221846	0.006921653 CHES1 checkpoint suppressor 1
25763	0.000129642 ANKH ankylosis, progressive (mouse) homolog
68950	3.39E-09 CCNE1 cyclin E1
788309	0.035143688 RMP RPB5-mediating protein
730410	0.001453479 LCK lymphocyte-specific protein tyrosine kinase
503725	0.010812215 ESTs
346688	0.001091951 MIA melanoma inhibitory activity
2306860	0.000346451 MAD2L2 MAD2 (mitotic arrest deficient, yeast, homolog)-like 2
782428	0.044484074 C1orf16 chromosome 1 open reading frame 16
242037	6.76E-06 FLJ20746 hypothetical protein
358052	0.005746627 ESTs
1946448	2.88E-05 CAV2 caveolin 2
2046118	2.22E-06 RAD54L RAD54 (S.cerevisiae)-like
1471841	0.000169912 ATP1A1 ATPase, Na+/K+ transporting, alpha 1 polypeptide
824510	0.00041118 LOC51647 CGI-128 protein
141806	0.002003247 TNFAIP3 tumor necrosis factor, alpha-induced protein 3
486110	0.004730919 PFN2 profilin 2
1586124	3.20E-05 FLJ11413 hypothetical protein FLJ11413

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840556	0.00087773 EIF4EL3 eukaryotic translation initiation factor 4E-like 3
1589468	0.001850652 EMP1 epithelial membrane protein 1
2019376	0.03681114 MGC2718 hypothetical protein MGC2718
346696	0.021270804 TEAD4 TEA domain family member 4
796197	6.83E-06 DMD dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272
796198	0.004000613 EFNB2 ephrin-B2
731080	2.98E-05 FLJ12661 hypothetical protein FLJ12661
324772	0.042068695 LCCP Leman coiled-coil protein
950690	0.035127941 CCNA2 cyclin A2
841501	2.51E-07 KIAA0102 KIAA0102 gene product
1466237	0.002257726 TES testis derived transcript (3 LIM domains)
1457416	0.004076409 KIAA0728 KIAA0728 protein
153977	0.00188129 POP4 POP4 (processing of precursor, S. cerevisiae) homolog
840567	0.000523423 TM4SF1 transmembrane 4 superfamily member 1
768000	0.000909544 RNASEH1 ribonuclease H1
341763	0.044284858 CASP5 caspase 5, apoptosis-related cysteine protease
768007	1.46E-07 CL683 weakly similar to glutathione peroxidase 2
768008	0.000389422 BAG2 BCL2-associated athanogene 2
39833	9.83E-05 CPVL carboxypeptidase, vitellogenic-like
843110	0.0039532 GDI1 GDP dissociation inhibitor 1
155583	0.034919482 TRAF1 TNF receptor-associated factor 1
810485	0.000238475 ID1 inhibitor of DNA binding 1, dominant negative helix-loop-helix protein
767068	4.46E-13 DKFZP586G1517 DKFZP586G1517 protein
108801	3.53E-05 FLJ20392 hypothetical protein FLJ20392
290866	1.21E-06 RAF1 v-raf-1 murine leukemia viral oncogene homolog 1
1604703	0.009410539 HLA-F major histocompatibility complex, class I, F
1584540	0.000352001 Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022)
1590021	3.88E-07 ETV6 ets variant gene 6 (TEL oncogene)
204897	6.91E-07 PLCG2 phospholipase C, gamma 2 (phosphatidylinositol-specific)
769751	2.75E-07 KIAA0095 KIAA0095 gene product
430928	0.005339331 BARD1 BRCA1 associated RING domain 1

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823598	0.029081002 PSMD12 proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
843121	0.000124807 CLIC1 chloride intracellular channel 1
139558	0.008816 Homo sapiens gastric cancer-related protein GCYS-20 (gcys-20) mRNA, complete cds
843126	0.010510953 S1PL S1PL protein
753313	0.002864496 LAPTM5 Lysosomal-associated multispinning membrane protein-5
175123	0.037853387 MAPK7 mitogen-activated protein kinase 7
824547	0.000238959 MHC2TA MHC class II transactivator
1592715	1.98E-05 HOMER-3 Homer, neuronal immediate early gene, 3
272155	0.006067385 SRGAP2 KIAA0456 protein
1845169	0.006064365 RAB35 RAB35, member RAS oncogene family
489489	2.07E-07 LBR lamin B receptor
629542	0.002987142 MYH1 myosin, heavy polypeptide 1, skeletal muscle, adult
490023	1.39E-05 WNT5B wingless-type MMTV integration site family, member 5B
2430676	0.039914681 EZFIT endothelial zinc finger protein induced by tumor necrosis factor alpha
868396	1.13E-05 LOC64148 17kD fetal brain protein
782460	0.009363602 Homo sapiens cDNA FLJ10500 fis, clone NT2RPP2000369
1948085	0.000313027 CBR3 carbonyl reductase 3
235938	0.009238649 BAK1 BCL2-antagonist/killer 1
897822	0.003765884 SYK spleen tyrosine kinase
586803	7.34E-08 PGF placental growth factor, vascular endothelial growth factor-related protein
746105	4.10E-05 LTRPC7 homolog of mouse transient receptor potential-phospholipase C-interacting kinase Chak; hypothetical protein FLJ20117
2271240	0.001624493 RPS12 ribosomal protein S12
32231	0.000744224 FLJ12442 hypothetical protein FLJ12442
1394099	0.000187841 MGC5528 hypothetical protein MGC5528
202514	0.000114404 DNMT3A DNA (cytosine-5)-methyltransferase 3 alpha
788355	0.001475302 STAG3 stromal antigen 3
815737	3.71E-09 ATP5A1 ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle
726582	1.36E-05 ARP3BETA actin-related protein 3-beta
244764	0.001161294 B7-H3 B7 homolog 3
814798	2.03E-08 ALDH1A3 aldehyde dehydrogenase 1 family, member A3

854644	0.011182578 NPC2 Niemann-Pick disease, type C2 gene
2011138	0.001310947 KIAA1036 KIAA1036 protein
194804	0.0121963 PITPN phosphatidylinositol transfer protein
209066	0.001333458 STK15 serine/threonine kinase 15
121530	0.023976232 MGC10966 hypothetical protein MGC10966
430954	9.12E-06 FLJ22341 hypothetical protein FLJ22341
687054	0.016868879 RELB v-rel avian reticuloendotheliosis viral oncogene homolog B (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3)
624627	0.004546557 RRM2 ribonucleotide reductase M2 polypeptide
357450	0.030931622 MTR Mouse Mammary Tumor Virus Receptor homolog
25030	0.006951821 PCMF potassium channel modulatory factor
756687	0.004407309 CD36L1 CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1
666879	4.67E-06 ANXA8 annexin A8
68225	0.036628745 Homo sapiens pTm5 mariner-like transposon mRNA, partial sequence
486175	0.0005382 SLC16A1 solute carrier family 16 (monocarboxylic acid transporters), member 1
796539	0.000602202 TRIL28 tripartite motif-containing 28
745189	9.02E-05 DAZAP1 DAZ associated protein 1
810813	0.001864702 S100A2 S100 calcium-binding protein A2
486179	0.000858947 NFAT5 nuclear factor of activated T-cells 5, tonicity-responsive
149355	0.011544468 TRAM translocating chain-associating membrane protein
1476053	0.03289313 RAD51 RAD51 (S. cerevisiae) homolog (E coli RecA homolog)
2062507	2.18E-07 KLF5 Kruppel-like factor 5 (intestinal)
1634832	0.026304968 WSX-1 class I cytokine receptor
1420842	0.01376248 MAL T1 mucosa associated lymphoid tissue lymphoma translocation gene 1
489805	0.028082851 HSF4 heat shock transcription factor 4
611532	7.05E-06 TNNI2 troponin I, skeletal, fast
796542	8.87E-05 ETV5 ets variant gene 5 (ets-related molecule)
727551	1.40E-08 IRF2 interferon regulatory factor 2
50987	0.016625494 PABPC4 poly(A)-binding protein, cytoplasmic 4 (inducible form)
823925	0.001754502 LOC51177 CK2 interacting protein 1; HQ0024c protein
121551	1.86E-08 LAD1 ladinin 1
869375	0.003859746 IDH2 isocitrate dehydrogenase 2 (NADP+), mitochondrial

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022041001010PC	
73852	0.017664041 Homo sapiens cDNA FLJ14388 fis, clone HEMBA1002716
252953	0.019402013 GS3786 predicted osteoblast protein
2321529	0.026304832 KCNG1 potassium voltage-gated channel, subfamily G, member 1
1476065	0.000528763 STMN1 stathmin 1/oncoprotein 18
854678	0.015997677 DKFZP566J091 hypothetical protein DKFZp566J091
196435	0.00388413 ESTs, Weakly similar to KIAA0738 protein [H.sapiens]
843174	0.001025358 PGM1 phosphoglucomutase 1
52594	0.036156197 PCDH8 protocadherin 8
20115	0.021509161 SLC9A6 solute carrier family 9 (sodium/hydrogen exchanger), isoform 6
669443	0.003570072 HSF2 heat shock transcription factor 2
770355	0.014696243 LSS lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
51947	0.025874177 Homo sapiens, clone M13C:20842 IMAGE:4542449, mRNA, complete cds
809503	0.001947255 ESTs, Weakly similar to AC004858.3 U1 small ribonucleoprotein 1 SNRP homolog [H.sapiens]
193106	0.003498139 ATP5G3 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3
1702742	2.07E-07 SLCTA5 solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
815781	0.046183854 HSP105B heat shock 105kD
782800	0.046687885 UQCRCF1 ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
68259	0.000734236 RENT2 regulator of nonsense transcripts 2
121577	1.83E-06 FLJ22393 hypothetical protein FLJ22393
1912458	1.43E-08 IL12A interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)
70533	0.00154863 HPS Hermansky-Pudlak syndrome
1660666	0.017638942 CA5B carbonic anhydrase VB, mitochondrial
51950	0.002759641 AQP1 aquaporin 1 (channel-forming integral protein, 28kD)
291880	2.95E-05 MFAP2 microfibrillar-associated protein 2
1555478	0.031251603 ST2 syntenin-2 protein
51955	1.54E-08 FLJ22282 hypothetical protein FLJ22282
79761	0.038130306 TMPO thymopoietin
843195	0.005767924 PSPH phosphoserine phosphatase
292388-2	0.000484852 LOC55977 hypothetical protein 24636
246704	0.013447399 RAI RelA-associated inhibitor
782811	6.86E-07 HMG1Y high-mobility group (nonhistone chromosomal) protein isoforms I and Y

022041001010PC	
271568	0.000866786 ACTR3 ARP3 (actin-related protein 3, yeast) homolog
2307119	2.37E-06 INFP4A inositol polyphosphate-4-phosphatase, type I, 107KD
838662	0.010070202 HCNPG transcriptional regulator protein
810859	0.047573891 NK4 natural killer cell transcript 4
241481	0.014557615 CASP10 caspase 10, apoptosis-related cysteine protease
2094232	5.18E-06 EGLN1 EGL nine (C.elegans) homolog 1
267691	0.007853541 FLJ20360 hypothetical protein FLJ20360
788705	0.018859374 USF1 upstream transcription factor 1
592359	0.037494688 HKE4 HLA class II region expressed gene KE4
2159983	3.25E-08 POIRMIN pro-oncosis receptor inducing membrane injury gene
2016426	0.009898035 KIAA0664 KIAA0664 protein
270917	3.65E-08 SFFP1 secreted frizzled-related protein 1
625623	0.001515188 Homo sapiens mRNA; cDNA DKFZp434F152 (from clone DKFZp434F152)
1492426	0.000486718 C19orf3 chromosome 19 open reading frame 3
1556433	0.013873827 GRO3 GRO3 oncogene
2010543	0.000219946 DD28 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 28
1466621	0.023035247 ATP2C1 ATPase, Ca++ transporting, type 2C, member 1
299388	1.27E-06 PP15 nuclear transport factor 2 (placental protein 15)
146966	0.002597189 DLL3 delta-like 3 (Drosophila)
771323	6.28E-10 PLOD procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI)
306444	0.011573645 TAF11 TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28 kD
382654	0.005845554 PCSK2 proprotein convertase subtilisin/kexin type 2
544639	1.14E-07 ESTs
306446	0.001825487 C11orf24 chromosome 11 open reading frame 24
838676	0.017828051 CAPN6 calpain 6
42070	0.000619438 NT5 5' nucleotidase (CD73)
809530	0.009640123 MCM2 minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin)
754346	2.60E-05 ESTs, Weakly similar to B49647 GTP-binding protein rab8 [H.sapiens]
882402	0.003800629 KIAA0692 KIAA0692 protein
770388	0.004124332 CLDN4 claudin 4
815015	0.000124184 TERA TERA protein

022041001010PC	
1604005	1.58E-05 SH3KBP1 SH3-domain kinase binding protein 1
789376	0.02515722 TXNRPD1 thioredoxin reductase 1
814072	0.000473 Homo sapiens, clone MGC:19517 IMAGE:4335816, mRNA, complete cds
504791	0.004943728 GSTA4 glutathione S-transferase A4
3220641	0.018173943 OR7E24P olfactory receptor, family 7, subfamily E, member 24 pseudogene
325033	0.016712654 ESTs
814076	0.01354434 NSAP1 NS1-associated protein 1
811817	0.009457359 FLJ21032 hypothetical protein FLJ21032
510273	0.030089117 PLEC1 plectin 1, intermediate filament binding protein, 500kD
377048	0.000173284 MYO1B myosin 1B
1034776	0.000124401 AD037 AD037 protein
322494	1.89E-05 CBFEB core-binding factor, beta subunit
46367	0.001719417 CHK choline kinase
1519143	0.000508533 RISC likely homolog of rat and mouse retinoid-inducible serine carboxypeptidase
789382	0.029514943 NOTCH4 Notch (Drosophila) homolog 4
263716	0.003686053 COL6A1 collagen, type VI, alpha 1
823982	0.00726442 TRIM26 tripartite motif-containing 26
140197	0.004538178 LOC51299 neuritin
786048	0.000316752 E2F4 E2F transcription factor 4, p107/p130-binding
1947804	0.014717852 TREX1 three prime repair exonuclease 1
414939	0.00278887 ETV4 ets variant gene 4 (E1A enhancer-binding protein, E1AF)
279085	0.012204566 MYO9B myosin IXB
259842	2.42E-05 PMPCB peptidase (mitochondrial processing) beta
232697	0.003201006 TIMM10 translocase of inner mitochondrial membrane 10 (yeast) homolog
809557	0.006003565 MCM3 minichromosome maintenance deficient (S. cerevisiae) 3
725223	1.33E-05 KIAA0077 KIAA0077 protein
840978	6.56E-06 CD81 CD81 antigen (target of antiproliferative antibody 1)
490414	2.13E-08 C2orf2 chromosome 2 open reading frame 2
786053	0.038091532 Homo sapiens cDNA FLJ30898 fis, clone FEBRA200572
564981	2.34E-05 Homo sapiens, Similar to RIKEN cDNA 2810433K01 gene, clone MGC:10200 IMAGE:3909951, mRNA, complete cds
810899	9.04E-06 ESTs

022041001010PC

288999	0.000887435 SPEC1 small protein effector 1 of Cdc42
1473876	4.29E-05 KIAA0187 KIAA0187 gene product
796904	1.58E-05 PLAGL1 pleiomorphic adenoma gene-like 1
344720	0.001678075 GYPC glycophorin C (Gerbich blood group)
1534544	0.004653836 PCCX2 protein containing CXXC domain 2
126858	0.038264032 SOAT1 sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1
202904	0.00238904 SFRS7 splicing factor, arginine/serine-rich 7 (35kD)
840984	0.004457062 CAV2 caveolin 2
138672-2	5.39E-06 ESTs
882439	0.017638691 CPR2 cell cycle progression 2 protein
2721773	0.027704333 NOG noggin
786067	8.88E-05 CDC25B cell division cycle 25B
1575059	0.028270162 TBC1C tubulin-specific chaperone c
1947827	0.01489065 MSTP028 MSTP028 protein
2390593	4.77E-06 PTFN14 protein tyrosine phosphatase, non-receptor type 14
767487	5.80E-05 ARIH1 ariadne (Drosophila) homolog, ubiquitin-conjugating enzyme E2-binding protein, 1
161484	4.46E-05 DGAT2 diacylglycerol O-acyltransferase homolog 2 (mouse)
2052032	1.96E-07 MYO10 myosin X
712139	2.31E-09 ARL7 ADP-ribosylation factor-like 7
770709	0.000831262 KIAA1089 KIAA1089 protein
2017415	1.21E-05 CENPA centromere protein A (17kD)
740620	2.38E-05 TPM2 tropomyosin 2 (beta)
184354	6.99E-07 EST
182750	0.012645421 MSI1 Musashi (Drosophila) homolog 1
76481	0.024566797 PTK9L protein tyrosine kinase 9-like (A6-related protein)
785417	0.011581406 NCUBE1 non-canonical ubiquitin conjugating enzyme 1
2313732	0.002401111 PLAA phospholipase A2-activating protein
1911864	0.005343697 GNG4 guanine nucleotide binding protein 4
503096	1.97E-05 ESTs
810119	3.53E-05 SNAI1 snail 1 (drosophila homolog), zinc finger protein
713886	0.018673346 CNN2 calponin 2
281392	0.005737829 Homo sapiens mRNA; cDNA DKFZp761G02121 (from clone DKFZp761G02121); partial cds

431214	0.005427358 FLJ12484 hypothetical protein FLJ12484
205185	0.010013706 THBD thrombomodulin
813460	0.005587928 PCSK7 proprotein convertase subtilisin/kexin type 7
809588	0.022949968 GGH gamma-glutamyl hydrolase (conjugase, folypolygammaglutamyl hydrolase)
1901310	0.001063475 KIAA1209 KIAA1209 protein
257197	0.005064867 NRB1-2 nuclear receptor binding factor-2
502446	0.004574652 DKFZP564A2416 DKFZP564A2416 protein
156962	0.016124526 ESTs
882459	0.007855578 PPIC peptidylprolyl isomerase C (cyclophilin C)
588822	0.000420841 COVA1 cytosolic ovarian carcinoma antigen 1
625683	4.54E-05 NOC4 neighbor of COX4
470128	2.92E-08 MYO1E myosin 1E
233679	2.38E-05 FLJ22362 hypothetical protein FLJ22362
683177	0.016770876 MAP4K5 mitogen-activated protein kinase kinase kinase kinase 5
700792	0.026756579 CDKN3 cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)
882461	0.001070887 ASS argininosuccinate synthetase
1518538	0.000295474 MGC4607 hypothetical protein MGC4607
1517595	2.27E-06 KIAA0175 likely ortholog of maternal embryonic leucine zipper kinase
950355	0.000138935 ESTs, Weakly similar to TRHY_HUMAN TRICHOHYALIN [H.sapiens]
839682	4.07E-06 UBE2N ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)
625693	0.001165816 MGC10911 hypothetical protein MGC10911
289978	0.00024508 UBL4 ubiquitin-like 4
25440	0.003949353 STAU2 stauflen (Drosophila, RNA-binding protein) homolog 2
346360	0.039034227 LAT linker for activation of T cells
1161155	0.000197727 CDKN2A cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)
2028949	0.034919482 PRO1855 hypothetical protein PRO1855
1925939	0.025350497 PLAGL2 pleiomorphic adenoma gene-like 2
32664	0.045777709 GNAO1 guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O
1542749	3.27E-08 AMD1 S-adenosylmethionine decarboxylase 1
2316305	0.000257732 DKFZP566D213 DKFZP566D213 protein
724615	0.00452876 CHC1 chromosome condensation 1
951304	0.011615484 KIAA0573 KIAA0573 protein

022041001010PC

75859	4.68E-06 NDRG2 N-myc downstream-regulated gene 2
950361	0.002582165 EST
898122	0.003101713 C7 complement component 7
898123	1.31E-05 GART phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
1881171	0.00258728 ESTs
594322	0.014086588 PAPSS1 3'-phosphoadenosine 5'-phosphosulfate synthase 1
530958	0.000152832 SMCH smoothened (Drosophila) homolog
813490	7.09E-07 CORO1C coronin, actin-binding protein, 1C
2308153	0.003570072 ELL ELL gene (1'-19 lysine-rich leukemia gene)
785459	0.001112368 SMTN smoothelin
767817	7.55E-07 POLR2F polymerase (RNA) II (DNA directed) polypeptide F
153650	0.001255544 KIAA1140 KIAA1140 protein
810156	0.007406628 DTYMK deoxythymidylate kinase (thymidylate kinase)
1035796	0.00021094 ESTs, Weakly similar to T33068 hypothetical protein C35E7.9 - <i>Caenorhabditis elegans</i> [C.elegans]
811897	0.002192122 MKL1 megakaryoblastic leukemia (translocation) 1
824203	0.018221151 DNCL12 dynein, cytoplasmic, light intermediate polypeptide 2
744952	0.024481266 ESTs, Moderately similar to UQHUR7 ubiquitin / ribosomal protein S27a, cytosolic [H.sapiens]
85634	0.000676725 C1S complement component 1, s subcomponent
132395	0.008012849 SRRM1 serine/arginine repetitive matrix 1
2012523	6.10E-07 FABP5 fatty acid binding protein 5 (psoriasis-associated)
773301	3.74E-12 CDH3 cadherin 3, type 1, P-cadherin (placental)
811108	0.000222819 TRIF6 thyroid hormone receptor interactor 6
416959	1.42E-08 NFIB nuclear factor I/B
250699	0.019002987 Homo sapiens, clone IMAGE:3888869, mRNA, partial cds
144849	3.25E-08 CLP coactosin-like protein
743220	0.000600627 FLJ12517 hypothetical protein FLJ12517
283328	0.000987968 EST
842939	0.022592867 ADARB1 adenosine deaminase, RNA-specific, B1 (homolog of rat RED1)
417905	0.00632472 Homo sapiens, Similar to RIKEN cDNA 5730528L13 gene, clone MGC:17337 IMAGE:4213591, mRNA, complete cds
809918	0.000355143 FLJ21047 hypothetical protein FLJ21047

022041001010PC	
811116	0.027129738 Homo sapiens, clone IMAGE:3632168, mRNA
2014138	0.003381521 FACL2 fatty-acid-Coenzyme A ligase, long-chain 2
309092	3.07E-05 APG5L APG5 (autophagy 5, S. cerevisiae)-like
128811	0.000579172 MGC2452 hypothetical protein MGC2452
768496	0.011680975 EB13 Epstein-Barr virus induced gene 3
772373	0.001284654 Homo sapiens cDNA FLJ30865 fis, clone FEBRA2004099
140574	4.08E-13 SCYD1 small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)
263013	0.000365845 PLOD2 procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2
2161427-2	0.000159834 PGR progesterone receptor
1606790	0.002826291 MGC12217 hypothetical protein MGC12217
1509761	1.92E-06 KRTHB6 keratin, hair, basic, 6 (monilethrix)
469924	0.00156327 PCTP phosphatidylcholine transfer protein
724652	0.000324169 CD8B1 CD8 antigen, beta polypeptide 1 (p37)
773322	0.001724267 SHOX2 short stature homeobox 2
773324	0.00075407 FLJ10439 hypothetical protein FLJ10439
711552	0.004197328 CBR1 carbonyl reductase 1
773329	0.003063069 KIAA1204 KIAA1204 protein
1422894	0.01526361 NOTCH2 Notch (Drosophila) homolog 2
2010949	0.000264549 ME2 malic enzyme 2, NAD(+)-dependent, mitochondrial
897509	0.000195032 ESTs, Weakly similar to S23650 retrovirus-related hypothetical protein II [H.sapiens]
223176	0.004691656 MAD MAX dimerization protein
744980	0.029325674 KIAA0304 KIAA0304 gene product
1518591	0.000137744 EST
784830	0.0001858 D123 D123 gene product
431280	0.000580358 EST
246041	0.00099919 MRPS35 mitochondrial ribosomal protein S35
25499	0.031951505 DKFZp564A176 hypothetical protein DKFZp564A176
505059	0.017104301 HSD11B1 hydroxysteroid (11-beta) dehydrogenase 1
377441	0.000151691 S100A3 S100 calcium-binding protein A3
80727	3.81E-05 ROR1 receptor tyrosine kinase-like orphan receptor 1
814478	0.009751136 BCL2A1 BCL2-related protein A1
714106	0.003765884 PLAU plasminogen activator, urokinase

022041001010PC

773330	0.000805296 GPNMB glycoprotein (transmembrane) nmb
343079	0.044429786 Homo sapiens mRNA; cDNA DKFZp761P0114 (from clone DKFZp761P0114)
773331	1.90E-05 ESTs, Weakly similar to YK61_YEAST HYPOTHETICAL 39.6 KDA PROTEIN IN MTD1-NUP133 INTERGENIC REGION [S.cerevisiae]
324492	0.029371795 MMP3 matrix metalloproteinase 3 (stromelysin 1, progelatinase)
132711	5.39E-08 KLF5 Kruppel-like factor 5 (intestinal)
841226	0.005177763 NS1-BP NS1-binding protein
842968	0.000543163 BUE1B budding uninhibited by benzimidazoles 1 (yeast homolog), beta
795263	0.004420295 FLJ22638 hypothetical protein FLJ22638
2309141	0.007213754 CD97 CD97 antigen
950700	0.002257726 PP pyrophosphatase (inorganic)
725618	0.007582436 Homo sapiens mRNA containing (CAG) ₄ repeat, clone CZ-CAG-7
1655480	0.00653861 ESTs
377452	0.037494688 LOC55818 putative zinc finger protein
845513	0.000814278 AP47 clathrin-associated protein AP47
811149	0.002784531 C9orf3 chromosome 9 open reading frame 3
160126	0.009121318 COX10 COX10 (Yeast) homolog, cytochrome c oxidase assembly protein (heme A: farnesyltransferase)
144880	8.33E-05 LOC56932 hypothetical protein from EUROIMAGE 1759349
144881	0.000416861 CALU calumenin
845519	0.002618542 ATP5C1 ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1
884425	0.01173607 CCT5 chaperonin containing TCP1, subunit 5 (epsilon)
950710	3.51E-06 PCCA propionyl Coenzyme A carboxylase, alpha polypeptide
2013515	6.64E-07 SGK serum/glucocorticoid regulated kinase
1869486	0.001399452 PRKX protein kinase, X-linked
897531	4.76E-06 MCAM melanoma cell adhesion molecule
782176	0.001737318 LOC136442 similar to MRJ gene for a member of the DNAJ protein family (H. sapiens)
703707	8.41E-06 ASPH aspartate beta-hydroxylase
154657	0.030945971 Homo sapiens cDNA: FLJ21286 fis, clone COL01915
753034	0.006100942 NFIX nuclear factor I/X (CCAAT-binding transcription factor)
753038	3.93E-06 KIFC3 kinesin family member C3
795280	0.017638942 ESTs
628602	0.003953106 MYL3 myosin, light polypeptide 3, alkali; ventricular, skeletal, slow

022041001010PC

813841	0.00266223 PLAT plasminogen activator, tissue
785804	0.000661605 CECR5 cat eye syndrome chromosome region, candidate 5
73531	2.64E-07 NIFU nitrogen fixation cluster-like
271219	0.010004815 Homo sapiens cDNA FLJ12566 fis, clone NT2RM4000852
1879255	0.021427151 DPYSL4 dihydropyrimidinase-like 4
1913855	0.005854823 MRPS17 mitochondrial ribosomal protein S17
345787	1.23E-05 HEC highly expressed in cancer, rich in leucine heptad repeats
810504	0.020902723 PLP2 proteolipid protein 2 (colonic epithelium-enriched)
811161	0.000316188 ABCF1 ATP-binding cassette, sub-family F (GCN20), member 1
1556872	0.012702024 FLJ12628 hypothetical protein FLJ12628
897542	9.81E-05 DKFZP564F0522 DKFZP564F0522 protein
282720	0.02278302 OIP2 Opa-interacting protein 2
897544	0.02996845 LMNA lamin A/C
757328	0.002130274 FLJ22678 hypothetical protein FLJ22678
589869	2.56E-07 TAZ transcriptional co-activator with PDZ-binding motif (TAZ)
1474149	0.042782235 PVRL1 poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin)
789012	0.000225033 FBLN2 fibulin 2
842994	0.002759641 CTSZ cathepsin Z
249705	0.037596341 DSS1 Deleted in split-hand/split-foot 1 region
2028238	0.000866786 KIAA0300 KIAA0300 protein
530237	0.012438932 Homo sapiens cDNA FLJ14208 fis, clone NT2RP3003264
664975	0.008779706 CLDN1 claudin 1
70201	3.09E-06 LOC51312 mitochondrial solute carrier
340850	0.0041899 MGC12992 hypothetical protein MGC12992
191978	5.46E-05 ATP5J2 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2
782193	0.002728134 TXN thioredoxin
485220	7.62E-05 HSA011916 hypothetical protein
2019426	3.13E-05 PTPNS1 protein tyrosine phosphatase, non-receptor type substrate 1
825229	0.001223619 MRPL11 mitochondrial ribosomal protein L11
809981	7.94E-07 GPX4 glutathione peroxidase 4 (phospholipid hydroperoxidase)
179163-2	0.029938789 GRIN2C glutamate receptor, ionotropic, N-methyl D-aspartate 2C
41869	0.034236898 FLJ11017 hypothetical protein FLJ11017

022041001010PC	
563673	0.008164837 ALDH7A1 aldehyde dehydrogenase 7 family, member A1
2714973	8.88E-05 GALNS galactosamine (N-acetyl)-6-sulfate sulfatase (Morquio syndrome, mucopolysaccharidosis type IVA)
1638827	0.015500819 RFP3S ret finger protein-like 3 antisense
295843	0.042020398 CYP27A1 cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1
156283	0.041270668 ESTs
307843	5.77E-07 PPP2CA protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
1474164	0.010013706 FLJ12886 hypothetical protein FLJ12886
289288	0.003697618 ATP2C1 ATPase, Ca++ transporting, type 2C, member 1
50693	0.000289561 FLJ20232 hypothetical protein
884462	0.000194201 DSCR1 Down syndrome critical region gene 1
338599	1.85E-05 NR3P nuclear receptor binding protein
279810	0.039210986 Homo sapiens mRNA; cDNA DKFZp564O1016 (from clone DKFZp564O1016)
1948119	0.001273848 GRAF GTPase regulator associated with the focal adhesion kinase pp125
292512	0.001680803 MLL3 myeloid/lymphoid or mixed-lineage leukemia 3
685182	0.00023067 CCT6A chaperonin containing TCP1, subunit 6A (zeta 1)
1636156	0.005363775 FLJ21709 hypothetical protein FLJ21709
1553560	2.41E-06 ESTs, Weakly similar to hyperpolarization-activated cyclic nucleotide-gated channel hHCN2 [H.sapiens]
471196	2.95E-13 ITM3 integral membrane protein 3
754018	0.000287497 SVIL supervillin
179163	0.013936342 GRIN2C glutamate receptor, ionotropic, N-methyl D-aspartate 2C
770059	0.002506551 HSPG2 heparan sulfate proteoglycan 2 (perlecan)
504461	0.00094691 OPN3 opsin 3 (encephalopsin, panopsin)
760298	0.018009132 PRSC1 protease, cysteine, 1 (legumain)
796268	0.010529568 PPP1R1A protein phosphatase 1, regulatory (inhibitor) subunit 1A
782501	0.000195601 PP1665 hypothetical protein PP1665
782503	0.015719214 FADS1 fatty acid desaturase 1
263097	0.000642521 RPIA ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase)
687875	0.027149103 CTSS cathepsin S
1733191	0.009227097 ESTs
771004	0.026126878 Homo sapiens, clone IMAGE:3880654, mRNA

1708335	0.005854823 GDF5 growth differentiation factor 5 (cartilage-derived morphogenetic protein-1)
756708	1.43E-08 KCNN4 potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4
1636166	0.000160656 KIAA0668 KIAA0668 protein
684539	0.011902794 Homo sapiens mRNA; cDNA DKFZp761E212 (from clone DKFZp761E212)
712577	0.000236843 HCCS holochochrome c synthase (cytochrome c heme-lyase)
754026	1.64E-09 SMURF2 E3 ubiquitin ligase SMURF2
1161564	9.84E-11 DMN desmuslin
429368	0.018119429 HOX11 homeo box 11 (T-cell lymphoma 3-associated breakpoint)
41898	0.005343697 PTGDS prostaglandin D2 synthase (21kD, brain)
810551	0.000677873 LRP1 low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)
812159	8.87E-05 FLJ20337 hypothetical protein FLJ20337
70245	0.011187375 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 50374
138672	7.63E-08 ESTs
1874367	0.019549691 SCYA20 small inducible cytokine subfamily A (Cys-Cys), member 20
49389	0.000722653 STX1A syntaxin 1A (brain)
897590	0.036633129 NESP55 neuroendocrine secretory protein 55
824602	0.014186983 IFI16 interferon, gamma-inducible protein 16
140951	4.83E-06 ACTN4 actinin, alpha 4
41108	0.039873583 Homo sapiens clone 25023 mRNA sequence
40164	0.008273187 Homo sapiens clone 23836 mRNA sequence
415613	0.042602065 LOC51304 DHHC1 protein
180803	0.01441978 INPP1 inositol polyphosphate-1-phosphatase
823665	0.000516552 PBEF pre-B-cell colony-enhancing factor
122238	0.013397185 KIAA0669 KIAA0669 gene product
502880	0.003571882 MGC11352 hypothetical protein MGC11352
812164	0.006694394 384D8-2 hypothetical protein 384D8_6
784129	0.003286809 YWHAG tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide
812167	0.045013394 GGA3 ADP-ribosylation factor-binding protein GGA3
810567	0.007408045 ARHGEF2 rho/rac guanine nucleotide exchange factor (GEF) 2
593001	4.44E-05 WHSC1 Wolf-Hirschhorn syndrome candidate 1
285323	0.000245162 ESTs, Weakly similar to A28996 proline-rich protein M14 precursor - mouse [M.musculus]

754040	6.62E-06 Homo sapiens cDNA FLJ31626 fis, clone NT2RI2003317
364716	0.000137407 MSH6 mutS (E. coli) homolog 6
193913	4.65E-09 LYN v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
205913	4.76E-05 FLJ10955 hypothetical protein FLJ10955
489553	0.014887446 ESRRRA estrogen-related receptor alpha
122241	0.000328148 PSMB2 proteasome (prosome, macropain) subunit, beta type, 2
360436	0.002697689 COPEB core promoter element binding protein
1584623	0.000523143 CCNC cyclin C
1914863	3.34E-10 DYSF dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)
2244561	0.026955181 CROCA transcriptional activator of the c-fos promoter
742685	0.000245162 DAB2 disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)
289615	0.008351255 LAMP2 lysosomal-associated membrane protein 2
1576468	0.001426413 HSD17B2 hydroxysteroid (17-beta) dehydrogenase 2
145112	0.009363602 ICAM1 intercellular adhesion molecule 1 (CD54), human rhinovirus receptor
756731	0.022873245 MAP3K3 mitogen-activated protein kinase kinase kinase 3
624390	0.000380341 DC13 DC13 protein
35642	0.007213754 FLJ10826 hypothetical protein FLJ10826
310034	5.32E-10 PRKY protein kinase, Y-linked
1846982	0.016285335 INHBC inhibin, beta C
825284	0.028295772 MGC5508 hypothetical protein MGC5508
868472	4.10E-08 CLIC4 chloride intracellular channel 4
327425	0.019017794 ESTs
2237353	0.021840957 GAL galanin
1911531	0.000758456 SH3GLB1 SH3-domain, GRB2-like, endophilin B1
345069	3.99E-06 NFE2L3 nuclear factor (erythroid-derived 2)-like 3
767164	2.48E-07 Homo sapiens cDNA FLJ32401 fis, clone SKMUS2000339
812187	0.029639799 MGC3279 hypothetical protein MGC3279 similar to collectins
758343	0.000196981 PPIF peptidylprolyl isomerase F (cyclophilin F)
780947	0.02676531 POLD1 polymerase (DNA directed), delta 1, catalytic subunit (125kD)
593023	0.008498512 DTN13 dystrobrevin, beta
209066-2	0.000805479 STK15 serine/threonine kinase 15
209137	3.88E-07 GABRE gamma-aminobutyric acid (GABA) A receptor, epsilon

022041001010PC	
1588924	0.001432315 HHGP HHGP protein
292567	0.000125692 MCPR anaphase-promoting complex 1; meiotic checkpoint regulator
44477	0.008204839 VCAM1 vascular cell adhesion molecule 1
1721076	3.74E-05 ZNF136 zinc finger protein 136 (clone pHZ-20)
825293	0.031216746 KIAA0082 KIAA0082 protein
840677	0.004604961 IGKC immunoglobulin kappa constant
768111	0.008346481 Homo sapiens mRNA; cDNA DKFZp586L0120 (from clone DKFZp586L0120)
769857	0.002264658 CBS cystathionine-beta-synthase
841620	0.000244327 DPYSL2 dihydropyrimidinase-like 2
855389	0.04294858 TACC1 transforming, acidic coiled-coil containing protein 1
28444	0.045698004 CRSP2 cofactor required for Sp1 transcriptional activation, subunit 2 (150kD)
43828	0.002262746 Homo sapiens, clone MGC:5564, mRNA, complete cds
42880	2.84E-07 CDK8 cyclin-dependent kinase 8
896978	0.00231445 FLJ12810 hypothetical protein FLJ12810
767180	0.000175172 C1orf6 chromosome 1 open reading frame 6
43833	0.001478693 DGKG diacylglycerol kinase, gamma (90kD)
207550	0.004415317 KIAA0057 TFRAM-like protein
188335	0.016029967 EMR2 egf-like module containing, mucin-like, hormone receptor-like sequence 1
276547	0.01022325 DNMT1 DNA (cytosine-5-)-methyltransferase 1
744605	0.000194318 FLJ10297 hypothetical protein FLJ10297
756769	0.000566667 CHAF1B chromatin assembly factor 1, subunit B (p60)
753428	0.016749826 Homo sapiens, Similar to RIKEN cDNA 1110014B07 gene, clone MGC:20766 IMAGE:4586039, mRNA, complete cds
344430	0.008499295 BMP7 bone morphogenetic protein 7 (osteogenic protein 1)
345090	0.006154605 GL004 GL004 protein
1622465	0.026837772 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
1917449	0.000329467 SA4A serum amyloid A4, constitutive
76182	0.000472307 DKFZP761F241 hypothetical protein DKFZp761F241
254625	0.010898804 KIAA0229 KIAA0229 protein
840697	0.040193056 FKBP9 FK506-binding protein 9 (63 kD)
255285	5.16E-09 ESTs

813157	7.60E-08 DKFZ547A023 hypothetical protein DKFZp547A023
259842-2	1.51E-06 PMPCB peptidase (mitochondrial processing) beta
782575	0.000103262 HSJ001348 cDNA for differentially expressed CO16 gene
612274	0.000642521 TUBA1 tubulin, alpha-1 (testis specific)
28469	0.015871 OXCT 3-oxoacid CoA transferase
1630639	0.043830461 ATP1A3 ATPase, Na+/K+ transporting, alpha-3 polypeptide
302996	0.022945273 CLIC3 chloride intracellular channel 3
378813	5.00E-10 SLP1 secretory leukocyte protease inhibitor (antileukoprotease)
782581	1.03E-05 KIAA0996 KIAA0996 protein
471568	8.73E-06 HNI1 hematological and neurological expressed 1
877621	0.013066696 AF9Q34 nGAP-like protein
746229	1.17E-13 MAP4K4 mitogen-activated protein kinase kinase kinase 4
265060	0.000287204 KIT v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
1632248	0.019761169 Homo sapiens cDNA FLJ14181 fis, clone NT2RP2004300
488956	0.002056402 CUGBP2 CUG triplet repeat, RNA-binding protein 2
591465	0.032429761 Homo sapiens, clone MGC:2908 IMAGE:3029644, mRNA, complete cds
2163910	0.021936941 CSFG3 chondroitin sulfate proteoglycan 3 (neurocan)
814117	0.01403347 DDX21 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21
769890	0.000279148 NP nucleoside phosphorylase
234325	0.006737438 CUL4A cullin 4A
45464	6.10E-07 AK2 adenylyate kinase 2
284734	0.044838359 WASF1 WAS protein family, member 1
843263	0.005565298 MRPL37 mitochondrial ribosomal protein L37
897956	0.000566151 PRAME preferentially expressed antigen in melanoma
282051	0.007261049 ESTs, Highly similar to [38945 melanoma ubiquitous mutated protein [H.sapiens]
744632	5.13E-08 EST
43865	1.57E-05 DNC11 dynein, cytoplasmic, intermediate polypeptide 1
841663	3.62E-05 NARF nuclear prelamins A recognition factor
1525461	0.001442019 RIPK2 receptor-interacting serine-threonine kinase 2
826286	0.002032859 IMP13 importin 13
1470278	0.000152832 FLJ21841 hypothetical protein FLJ21841
796646	6.57E-07 ODC1 ornithine decarboxylase 1

502161	0.001298549 APPBP1 amyloid beta precursor protein-binding protein 1, 59kD
1610338	0.021681051 FLJ22324 hypothetical protein FLJ22324
146123	0.003881514 PTPRK protein tyrosine phosphatase, receptor type, K
153340	0.009064405 GRO2 GRO2 oncogene
243155	0.048299748 FLJ12549 hypothetical protein FLJ12549
897963	6.59E-06 PPAP2A phosphatidic acid phosphatase type 2A
304908	1.10E-05 E2F3 E2F transcription factor 3
2701197	0.019362001 C11orf9 chromosome 11 open reading frame 9
119384	0.000965202 CHIT1 chitinase 1 (chitotriosidase)
877644	0.001738247 PRCC papillary renal cell carcinoma (translocation-associated)
220293	0.010938828 Homo sapiens cDNA: FLJ21800 fis, clone HEP00618
1732922	0.001365668 Homo sapiens mRNA; cDNA DKFZp762H106 (from clone DKFZp762H106)
470930	2.82E-05 DDX11 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase)
701460	0.001790158 CHFR checkpoint with forkhead and ring finger domains
269374	0.000195253 KIAA0301 KIAA0301 protein
825641	3.34E-06 B4GALT5 UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5
531608	0.002759613 HMGIC high-mobility group (nonhistone chromosomal) protein isoform I-C
300632	0.042347323 FLJ21044 hypothetical protein FLJ21044 similar to Rbig1
266037	0.00106935 MAFG v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein G
1585650	0.01494333 FLJ10781 hypothetical protein FLJ10781
841689	0.018506257 ATP6S1 ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump), subunit 1
1461477	1.32E-05 Homo sapiens mRNA; cDNA DKFZp586I0324 (from clone DKFZp586I0324)
784504	0.000195601 MBTPS1 membrane-bound transcription factor protease, site 1
1493160	0.001295674 SCYB10 small inducible cytokine subfamily B (Cys-X-Cys), member 10
47096	0.014632388 FUSIP2 FUS-interacting protein (serine-arginine rich) 2
770462	0.000758456 CPZ carboxypeptidase Z
745606	0.014811257 PP591 hypothetical protein PP591
268727	0.001267014 MUTYH mutY (E. coli) homolog
787851	0.042347323 Homo sapiens PRO2893 mRNA, complete cds
825659	0.006087414 NDRG1 N-myc downstream regulated
22917	0.013187912 Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)
1593829	0.044484074 TIA1 TIA1 cytotoxic granule-associated RNA-binding protein

022041001010PC	
111120	7.01E-06 KIAA0063 KIAA0063 gene product
810958	0.004710677 CPNE1 copine 1
950096	0.004536135 ARCN1 archain 1
853066	0.003225295 CNAP1 chromosome condensation-related SMC-associated protein 1
292936	4.65E-06 FLJ10468 hypothetical protein FLJ10468
701481	0.003482886 MX2 myxovirus (influenza) resistance 2, homolog of murine
897997	0.04142324 SMC1L1 SMC1 (structural maintenance of chromosomes 1, yeast)-like 1
136399	3.96E-05 DKFZP586F2423 hypothetical protein DKFZP586F2423
752837	4.76E-08 Homo sapiens mRNA for FLJ00074 protein, partial cds
278650-2	0.015052222 PPP1R8 protein phosphatase 1, regulatory (inhibitor) subunit 8
809627	0.000137744 NRIP1 nuclear receptor interacting protein 1
787860	2.92E-08 ESTs
183468	7.58E-08 EGFR epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)
416676	2.51E-09 PEL1 pellino (Drosophila) homolog 1
323522	8.66E-06 NRBP nuclear receptor binding protein
49794	0.005649538 LOC51700 cytochrome b5 reductase b5R.2
278504	0.036283521 KIAA0607 neurochondrin
951048	0.009825328 DKFZP434K046 hypothetical protein DKFZp434K046
460403	0.006497654 LAMC2 laminin, gamma 2 (nicein (100kD), kalinin (105kD), BM600 (100kD), Herlitz junctional epidermolysis bullosa)
124246	0.044429786 ESTs, Weakly similar to ALUC_HUMAN ALU CLASS C WARNING ENTRY [H.sapiens]
505836	0.00219195 ESTs, Moderately similar to reduced expression in cancer [H.sapiens]
796694	0.00244749 BIRC5 baculoviral IAP repeat-containing 5 (survivin)
811918	0.002709516 KIAA0952 KIAA0952 protein
1556545	0.012132745 Homo sapiens, Similar to RIKEN cDNA 2600001B17 gene, clone IMAGE:2822298, mRNA, partial cds
704045	4.14E-09 MGC4126 hypothetical protein MGC4126
1856063	0.013677014 TTYH1 tweety (Drosophila) homolog 1
276915	1.29E-05 DNMT3B DNA (cytosine-5)-methyltransferase 3 beta
211800	0.005621271 KIAA0833 KIAA0833 protein
232789	0.021224486 POLR2J polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)
277579	0.008167816 ESTs
813520	0.000287377 EPHB3 EphB3

022041001010PC	
486626	0.0454965 Homo sapiens, clone IMAGE:4332938, mRNA
882515	0.001000384 EIF3S9 eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD)
429799	0.031044349 FLJ21939 hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2
1569658	0.006181327 ESTs
1474900	0.043509438 KRT15 keratin 15
810983	0.001630467 DKFZP434H132 DKFZP434H132 protein
308163	0.018779849 ESTs, Weakly similar to TRHY_HUMAN TRICHOHYALIN [H.sapiens]
839736	7.03E-08 CRYAB crystallin, alpha B
1899263	0.04697029 FLJ20113 hypothetical protein FLJ20113
1536236	1.53E-14 FLJ13154 hypothetical protein FLJ13154
124261	0.010467742 SNRP70 small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen)
2018154	4.91E-07 ETFB electron-transfer-flavoprotein, beta polypeptide
67741	0.000180391 PP2135 PP2135 protein
266085	0.0003394 KHSRP KH-type splicing regulatory protein (FUSE binding protein 2)
825695	0.004394757 HSPC111 hypothetical protein
809657	0.013236102 Homo sapiens cDNA FLJ31373 fis, clone NB9N42000342
110507	0.000223108 ESTs, Weakly similar to T46471 hypothetical protein DKFZp434L0130.1 [H.sapiens]
724387	0.012976841 SNRPC small nuclear ribonucleoprotein polypeptide C
855786	0.002192122 WARS tryptophanyl-tRNA synthetase
259950	1.91E-05 CML66 chronic myelogenous leukemia tumor antigen 66
1899274	0.00024151 EGLN2 EGL nine (C.elegans) homolog 2
23903	0.020116819 Homo sapiens clone 23903 mRNA sequence
302292	0.005746627 EXT2 exostoses (multiple) 2
815142	0.000812059 SACS spastic ataxia of Charlevoix-Saguenay (sacsin)
505864	0.000602202 RGL RalGDS-like gene
325160	1.02E-11 NP25 neuronal protein
1868534	3.65E-05 MGC2408 hypothetical protein MGC2408
376515	0.00998974 FLJ10416 similar to constitutive photomorphogenic protein 1 (Arabidopsis)
136722	1.06E-05 ATP1B3 ATPase, Na ⁺ /K ⁺ transporting, beta 3 polypeptide
284022	0.001908121 ARHGEF10 Rho guanine nucleotide exchange factor (GEF) 10
2010684	0.009238649 KIAA0640 SWAP-70 protein
1739821	0.022220862 LOC83690 CocoaCrisp

1618987	0.008755709 RLBP1 retinaldehyde-binding protein 1
282428	0.003858041 Homo sapiens, Similar to RIKEN cDNA 9030409E16 gene, clone MGC:26939 IMAGE:4796761, mRNA, complete cds
1607482	5.44E-05 CE1PG CCAAT/enhancer binding protein (C/EBP), gamma
123627	0.012829341 P5 protein disulfide isomerase-related protein
1606829	0.005336709 HDAC4 histone deacetylase 4
81409	0.016588172 GABARAPL1 GABA(A) receptor-associated protein like 1
340558	0.000227672 ARPC5 actin related protein 2/3 complex, subunit 5 (16 kD)
1635970	1.87E-07 MFHAS1 malignant fibrous histiocytoma amplified sequence 1
454970	7.09E-05 HAIK1 type I intermediate filament cytokeleton
198509	0.034037336 NUDEL LIS1-interacting protein NUDEL; endooligopeptidase A
51328	0.000752302 CDC34 cell division cycle 34
41565	0.004757679 MYCN v-myc avian myelocytomatosis viral related oncogene, neuroblastoma derived
1691868	0.000858947 PTX3 pentaxin-related gene, rapidly induced by IL-1 beta
505881	0.006498381 ADA adenosine deaminase
813560	0.002137013 TRN-SR transportin-SR
505882	0.023035247 FLJ20550 hypothetical protein FLJ20550
469686	5.61E-06 RIT Ric (Drosophila)-like, expressed in many tissues
1493527	2.33E-05 ASNS asparagine synthetase
325182	0.027251157 CDH2 cadherin 2, type I, N-cadherin (neuronal)
784589	0.008673574 MMP15 matrix metalloproteinase 15 (membrane-inserted)
2579848	0.016470796 CHRA1 chromatin accessibility complex 1
854079	0.024580007 ACTN1 actinin, alpha 1
344854	2.86E-06 ANKRD3 ankyrin repeat domain 3
809696	0.0324664 DDX38 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 38
725365	0.015956866 GAS1 growth arrest-specific 1
713202	0.00119998 HSU79252 hypothetical protein
1723400	0.000511825 ESTs
950451	0.015225688 MGC10818 hypothetical protein MGC10818
844601	0.00263797 CCKBR cholecystokinin B receptor
502558	0.010898808 Homo sapiens, Similar to RIKEN cDNA 1110060O18 gene, clone MGC:17236 IMAGE:3864137, mRNA, complete cds

811976 0.002743023 Homo sapiens cDNA FLJ10071 fis, clone HEMBA1001702
 587992 0.000692211 MGC5350 | hypothetical protein MGC5350
 795309 1.99E-05 SOD3 | superoxide dismutase 3, extracellular
 486683 0.001570786 Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)
 768561 0.006003565 SCYA2 | small inducible cytokine A2 (monocyte chemotactic protein 1, homologous to mouse Sig-je)
 756401 0.008336499 RHEB2 | Ras homolog enriched in brain 2
 756405 0.014632388 ID3 | inhibitor of DNA binding 3, dominant negative helix-loop-helix protein
 144924 0.001209009 C6orf5 | chromosome 6 open reading frame 5
 768569 0.038661233 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1517766
 1688953 1.02E-07 ESTs
 144926 0.012004594 MGC3133 | hypothetical protein MGC3133
 594428 0.038751321 SEC3 | Sec3-like
 770848 0.00619877 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY Y J SEQUENCE CONTAMINATION WARNING
 429065 ENTRY [H.sapiens]
 1933127 0.00025476 ANKH | ankylosis, progressive (mouse) homolog
 1551675 4.99E-05 CX46.6 | connexin46.6
 30093 0.002246831 Homo sapiens cDNA FLJ13903 fis, clone THYRO1001854
 768571 3.59E-07 RANBP1 | RAN binding protein 1
 252382 2.06E-05 SOX8 | SRY (sex determining region Y)-box 8
 1493557 0.004755604 TM4SF6 | transmembrane 4 superfamily member 6
 144932 0.014557615 PRP18 | pre-mRNA processing factor 18
 705064 6.88E-09 CDK2AP1 | CDK2-associated protein 1
 391949 0.028746951 TACC3 | transforming, acidic coiled-coil containing protein 3
 1688965 7.81E-05 SH2D2A | SH2 domain protein 2A
 361861 0.016029967 Homo sapiens mRNA for putative NSE1 protein
 142259 0.000352001 PCBP4 | poly(C)-binding protein 4
 131839 0.001096449 FIP2 | tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin
 130892 interacting protein L; transcription factor IIIA-interacting protein
 2252417 0.000190493 FOLR1 | folate receptor 1 (adult)
 298122 0.000109361 EHD3 | EH-domain containing 3
 0.004138974 RPS10 | ribosomal protein S10
 0.003448915 FZD7 | frizzled (Drosophila) homolog 7

022041001010PC	
725390	2.24E-09 GSTP1 glutathione S-transferase pi
2308263	0.015071436 FDXR ferredoxin reductase
153760	4.24E-05 EPHB1 EphB1
713238	0.000107772 MCNDOA KIAA0867 protein
250797	0.034063029 FLJ20038 hypothetical protein FLJ20038
126221	0.001359734 TPD52L2 tumor protein D52-like 2
898249	0.001409555 ESTs
129569	0.000115962 HSPC049 HSPC049 protein
2115545	7.00E-05 ADCY7 adenylyate cyclase 7
269787	0.027049095 L1CAM L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs) syndrome, spastic paraplegia 1)
246120	0.008472265 HRMT1L2 HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2
415326	0.023366836 ESTs
868169	0.000993361 LPL lipoprotein lipase
1903066	7.49E-07 KRTHB1 keratin, hair, basic, 1
306933	0.036825 Homo sapiens clone 25012 mRNA sequence
773419	0.002212104 ESTs
758037	0.001366354 HIVEP1 human immunodeficiency virus type I enhancer-binding protein 1
308539	0.001531987 Homo sapiens cDNA FLJ12777 fis, clone NT2RFP2001720
1469377	9.20E-06 LHFP2 lipoma HMGIC fusion partner-like 2
898258	0.014789221 CHN1 chimerin (chimaerin) 1
841308	2.88E-07 MYLK myosin, light polypeptide kinase
815501	2.47E-08 MGC2721 hypothetical protein MGC2721
208969	0.000183624 EST
814562	0.003359378 ABT1 TATA-binding protein-binding protein
204686	0.015480089 FXYD1 FXYD domain-containing ion transport regulator 1 (phospholemman)
491545	0.001014724 KIAA0965 KIAA0965 protein
261518	2.50E-06 FLJ20287 hypothetical protein FLJ20287
154720	0.04010901 ARD1 N-acetyltransferase, homolog of S. cerevisiae ARD1
859359	5.91E-05 PIG3 quinone oxidoreductase homolog
2306682	0.028235912 AKAP9 A kinase (PRKA) anchor protein (yotiao) 9
756442	0.000637212 POR P450 (cytochrome) oxidoreductase

1388395	0.013736819 ELK1 ELK1, member of ETS oncogene family
770880	0.000953714 PRIM2A primase, polypeptide 2A (58kD)
770884	0.00070891 TIP-1 Tax interaction protein 1
788136	0.026617009 PDE4B phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)
1639531	0.000121707 RAB27A RAB27A, member RAS oncogene family
248829	0.000127033 LOX lysyl oxidase
28140	0.009335762 Homo sapiens mRNA; cDNA DKFZp586F2224 (from clone DKFZp586F2224)
50743	0.038854573 TXNL2 thioredoxin-like 2
884511	0.024982068 COX7B cytochrome c oxidase subunit VIIb
41929	0.015950143 PICALM phosphatidylinositol binding clathrin assembly protein
82434	0.021226526 EEF1G eukaryotic translation elongation factor 1 gamma
1574594	0.000255461 MDK midkine (neurite growth-promoting factor 2)
1031940	0.001333654 CAMP cathelicidin antimicrobial peptide
898281	8.51E-05 FLNA filamin A, alpha (actin-binding protein-280)
287749	9.83E-05 CDC7L1 CDC7 (cell division cycle 7, <i>S. cerevisiae</i> , homolog)-like 1
701115	1.56E-08 PRO2013 hypothetical protein PRO2013
283461	0.009028782 FLJ13910 hypothetical protein FLJ13910
188036	0.000166323 BPAG1 bullous pemphigoid antigen 1 (230/240kD)
196992	0.00144083 AKR1C1 aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)
150466	0.043662375 Homo sapiens cDNA FLJ14885 fis, clone PLACE1003711
760344	0.000228463 UMPS uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)
841338	0.000233667 PRNPIP prion protein interacting protein
509458	0.029325674 LOC57228 hypothetical protein from clone 643
132828	0.004269143 DSCR1L2 Down syndrome critical region gene 1-like 2
2015212	0.007053992 MRPS25 mitochondrial ribosomal protein S25
742707	1.36E-05 ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PRECURSOR [H.sapiens]
815534	0.000247752 ICAP-1A integrin cytoplasmic domain-associated protein 1
344134	0.00261847 IGLL1 immunoglobulin lambda-like polypeptide 1
795371	0.004029813 LSM5 U6 snRNA-associated Sm-like protein
261541	2.09E-09 PRKCN protein kinase C, nu

022041001010PC

24958	1.98E-06 Homo sapiens mRNA; cDNA DKFZp434C2016 (from clone DKFZp434C2016)
66406	4.34E-09 ESTs, Highly similar to T47163 hypothetical protein DKFZp762E1312.1 [H.sapiens]
2316471	1.76E-05 DEDD death effector domain-containing
22278	3.17E-05 FLJ20511 hypothetical protein FLJ20511
844680	0.01394813 TRD@ T cell receptor delta locus
1716265	0.001534143 WDR3 WD repeat domain 3
278938	0.009614286 LOC51144 steroid dehydrogenase homolog
177621	0.04563828 RXRB retinoid X receptor, beta
1642496	0.00087773 MGC11266 hypothetical protein MGC11266
796323	0.00106935 ADD3 adducin 3 (gamma)
50768	6.93E-06 DKFZp667O2416 hypothetical protein DKFZp667O2416
26566	1.26E-06 POWT1 protein-O-mannosyltransferase 1
1461138	0.029910221 H4FG H4 histone family, member G
130153	5.61E-06 SUPT5H suppressor of Ty (S.cerevisiae) 5 homolog
190325	0.000121317 Homo sapiens mRNA; cDNA DKFZp434E235 (from clone DKFZp434E235)
2149968	8.36E-07 FZD9 frizzled (Drosophila) homolog 9
767982	9.30E-07 Homo sapiens, clone IMAGE:4134852, mRNA, partial cds
51710	5.76E-07 Homo sapiens, clone IMAGE:3605655, mRNA
153025	0.00010788 LIF leukemia inhibitory factor (cholinergic differentiation factor)
773469	0.037388104 PTGFRN prostaglandin F2 receptor negative regulator
758088	8.07E-05 CALD1 caldesmon 1
823715	0.035143688 TRIP-B12 transcriptional regulator interacting with the PHS-bromodomain 2
26578	0.012675854 PES1 pescadillo (zebrafish) homolog 1, containing BRCT domain
815556	0.003550049 FLJ10430 hypothetical protein FLJ10430
810612	0.013015797 S100A11 S100 calcium-binding protein A11 (calgizzarin)
795395	0.037638089 MGC5306 hypothetical protein MGC5306
182177	0.031563977 ADAM17 a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)
155717	0.002588609 CD79B CD79B antigen (immunoglobulin-associated beta)
897650	0.000154041 PUS1 pseudouridylylate synthase 1
825320	0.031634717 Homo sapiens, clone IMAGE:3355383, mRNA, partial cds
1705861	0.003557075 KLK1 kallikrein 1, renal/pancreas/salivary

022041001010PC	
2055888	0.040566492 CENTG3 centaurin, gamma 3
161998	0.017117327 FLJ23138 hypothetical protein FLJ23138
265853	0.001192546 TEM8 tumor endothelial marker 8
2325609	0.001089545 MCM7 minichromosome maintenance deficient (S. cerevisiae) 7
774420	0.011363913 LMAN1 lectin, mannoside-binding, 1
324927	0.00185329 KIAA0375 KIAA0375 gene product
151449	9.30E-05 PTPN21 protein tyrosine phosphatase, non-receptor type 21
753162	0.005108161 KIAA0603 KIAA0603 gene product
897669	0.025225569 PRKCSH protein kinase C substrate 80K-H
2017930	0.020336469 KIP2 DNA-dependent protein kinase catalytic subunit-interacting protein 2
50794	0.011154216 ZNF133 zinc finger protein 133 (clone pHZ-13)
530359	0.013769878 FNTA farnesyltransferase, CAA box, alpha
785933	0.003257805 SRPX sushi-repeat-containing protein, X chromosome
731241	0.01978529 MPST mercaptopurivate sulfrtransferase
61500	1.32E-08 HLF hepatic leukemia factor
248886	0.020116819 RAB3-GAP150 rab3 GTPase-activating protein, non-catalytic subunit (150kD)
1416782	0.015739275 CKB creatine kinase, brain
154790	0.038568449 NGFR nerve growth factor receptor (TNFR superfamily, member 16)
969843	2.51E-09 ESTs, Weakly similar to LKHU proteoglycan link protein precursor [H.sapiens]
2062329	1.54E-08 TTK TTK protein kinase
1323636	0.001297059 MGAT1 mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase
27544	4.45E-11 PROML1 prominin (mouse)-like 1
825343	0.015128158 Homo sapiens, clone MGC:15887 IMAGE:3530481, mRNA, complete cds
41987	3.24E-06 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 966164
812244	0.00582367 CKLF1 chemokine-like factor 1
2321341	5.72E-06 PGC progastricsin (pepsinogen C)
1698036	0.030089117 UBE2V1 ubiquitin-conjugating enzyme E2 variant 1
855438	0.013975654 ATP6S14 ATPase, vacuolar, 14 kD
774446	0.000137487 ADM adrenomedullin
626068	0.025636692 XPOT exportin, tRNA (nuclear export receptor for tRNAs)
36374	0.008011127 CCNB1 cyclin B1
69002	0.000262283 ANGPTL4 angiopoietin-like 4

022041001010PC

531319	6.30E-08 STK12 serine/threonine kinase 12
1704155	0.046542451 IER5 immediate early response 5
753184	0.003943783 SOX9 SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal)
2032251	0.000446292 ESTs
34778	0.001089665 VEGF vascular endothelial growth factor
264146	0.008936352 FLJ13194 hypothetical protein FLJ13194
812256	0.01030915 Homo sapiens cDNA: FLJ21693 fis, clone COL09609
509800	0.008621514 CASK calcium/calmodulin-dependent serine protein kinase (MAGUK family)
712683	0.000116468 NCK1 NCK adaptor protein 1
2020898	0.012093702 PLCD3 procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3
1597813	0.001549458 PP1044 hypothetical protein PP1044
359982	0.008864958 BNIP3 BCL2/adenovirus E1B 19kD-interacting protein 3
1674521	0.026617009 EST
41208	3.23E-05 BMP1 bone morphogenetic protein 1
486304	5.01E-05 RASAL2 RAS protein activator ilke 2
2017960	0.001121595 PP1201 PP1201 protein
788507	0.046423899 ESTs, Weakly similar to LIN1_HUMAN LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]
327506	0.000554961 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 327506
753198	4.39E-09 JPO1 c-Myc target JPO1
769921	6.30E-05 UBE2C ubiquitin-conjugating enzyme E2C
201727	0.000831262 BCL6 B-cell CLL/lymphoma 6 (zinc finger protein 51)
2262296	0.012689251 MUC6 mucin 6, gastric
1568391	4.48E-10 PLS3 plaslin 3 (T isoform)
785963	0.00019309 KIAA0191 KIAA0191 protein
431759	0.043544579 TEAD3 TEA domain family member 3
785967	0.001744131 EPB41L2 erythrocyte membrane protein band 4.1-like 2
731279	0.015827676 HRB HIV-1 Rev binding protein
28510	0.000923428 CNTN2 contactin 2 (axonal)
838478	0.000657157 NCALD neurocalcin delta
36393	0.003553426 ACAT2 acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)
788511	0.022786019 RPS6KA1 ribosomal protein S6 kinase, 90kD, polypeptide 1
259627	4.41E-05 KIAA1126 KIAA1126 protein

840753	0.00460254 SCYA5 small inducible cytokine A5 (RANTES)
795730	0.000182825 EFS2 signal transduction protein (SH3 containing)
281145	0.006338467 AOC2 amine oxidase, copper containing 2 (retina-specific)
1894005	0.044484074 FLJ12615 hypothetical protein FLJ12615 similar to membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 5)
823775	0.000549733 GNAI3 guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3
774471	0.000851455 LAMB1 laminin, beta 1
454632	7.14E-08 KIAA0481 KIAA0481 gene product
323238	3.88E-05 GRO1 GRO1 oncogene (melanoma growth stimulating activity, alpha)
950897	0.001851412 Homo sapiens mRNA; cDNA DKFZp586G1922 (from clone DKFZp586G1922)
878330	0.037388104 Homo sapiens cDNA: FLJ22044 fis, clone HEP09141
755891	0.002132318 KIAA0317 KIAA0317 gene product
3172883	0.002068426 ESTs, Weakly similar to S24195 dopamine receptor D4 [H.sapiens]
358267	4.15E-05 ESTs, Moderately similar to AF119917 63 PRO2831 [H.sapiens]
230882	1.51E-06 PAX6 paired box gene 6 (aniridia, keratitis)
754157	3.44E-05 Homo sapiens mRNA; cDNA DKFZp434K2172 (from clone DKFZp434K2172)
1915913	0.006354505 CLIC2 chloride intracellular channel 2
788524	0.040583119 HSPC156 HSPC156 protein
282895	0.025901698 FLJ20048 hypothetical protein FLJ20048
795746	0.036395976 Homo sapiens cDNA FLJ33167 fis, clone UTERU2000569
1608898	1.20E-08 JRKL jerky (mouse) homolog-like
71312	0.000227672 UACA uveal autoantigen with coiled-coil domains and ankyrin repeats
162208	0.004091636 ARPC2 actin related protein 2/3 complex, subunit 2 (34 kD)
160609	0.000448621 ESTs, Weakly similar to ALUA_HUMAN !!! ALU CLASS A WARNING ENTRY !!! [H.sapiens]
136409	0.000809442 DKFZp547A023 hypothetical protein DKFZp547A023
1572298	0.046169524 CD3Z CD3Z antigen, zeta polypeptide (TIT3 complex)
460126	8.06E-07 KIAA0819 KIAA0819 protein
1049291	0.004674543 OR7E47P olfactory receptor, family 7, subfamily E, member 47 pseudogene
489677	0.000218116 UP uridine phosphorylase
814970	0.000351004 ELOVL1 elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1
795757	6.07E-05 FLJ11896 hypothetical protein FLJ11896
795758	0.001312689 DKFZp434B044 hypothetical protein DKFZp434B044

022041001010PC

1486770	0.001073614 FLJ10569 hypothetical protein FLJ10569
812294	0.001477658 ESTs
784257	0.001547684 KIF3C kinesin family member 3C
769959	2.17E-06 COL4A2 collagen, type IV, alpha 2
843321	2.31E-05 KR17 keratin 7
1350439	1.82E-11 KIAA0015 KIAA0015 gene product
767277	1.69E-05 PPIH peptidyl prolyl isomerase H (cyclophilin H)
2018941	2.34E-06 D21S2056E DNA segment on chromosome 21 (unique) 2056 expressed sequence
1755555	0.001985435 MAP3K6 mitogen-activated protein kinase kinase kinase 6
840788	0.008900276 TMSB10 thymosin, beta 10
814989	0.001107206 PPM1G protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform
172785	0.001708977 LOC51754 NAG-5 protein
1608120	0.0041899 AIB3 nuclear receptor coactivator RAP250; peroxisome proliferator-activated receptor interacting protein; thyroid hormone receptor binding protein
767289	0.038751321 KIAA1001 KIAA1001 protein
1926364	0.000305567 RBM9 RNA binding motif protein 9
346134	0.024280742 CRHSP-24 calcium-regulated heat-stable protein (24kD)
824753	0.000389422 FLJ22624 hypothetical protein FLJ22624
212198	3.41E-06 TP53BP2 tumor protein p53-binding protein, 2
813256	5.48E-07 ABCB1 ATP-binding cassette, sub-family B (MDR/TAP), member 1
1902841	0.001271788 SLC16A7 solute carrier family 16 (monocarboxylic acid transporters), member 7
415766	8.23E-06 KIAA1357 KIAA1357 protein
562409	0.022876597 NDUFS5 NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase)
48886	0.037983017 MRC1 mannose receptor, C type 1
713685	1.49E-06 PRSS2 protease, serine, 2 (trypsin 2)
233464	2.63E-06 EVA1 epithelial V-like antigen 1
2010393	0.001127212 FTSJ1 FtsJ homolog 1 (E. coli)
826363	3.96E-05 LYP1A2 lysophospholipase II
726791	0.016588172 EST00098 hypothetical protein EST00098
788568	0.003344334 ARHGGEF7 Rho guanine nucleotide exchange factor (GEF) 7
813265	4.16E-05 Homo sapiens mRNA: cDNA DKFZp564H1916 (from clone DKFZp564H1916)
289760	0.000134622 ESTs, Highly similar to T00391 hypothetical protein KIAA0612 [H.sapiens]

768246	0.000180794 Homo sapiens cDNA FLJ30869 fis, clone FEBRA2004224
783629	0.002812591 HUMAUANTIG nucleolar GTPase
2322367	2.80E-05 RTN4 reticulation 4
837870	0.001262114 PRELP proline arginine-rich end leucine-rich repeat protein
1690915	0.005767924 ESTs
220372	0.000449552 HS3ST1 heparan sulfate (glucosamine) 3-O-sulfotransferase 1
140328	0.000370802 ESTs
361539	0.002866566 Homo sapiens sortilin 1 (SORT1), mRNA
84464	0.00852718 FLJ12806 hypothetical protein FLJ12806
2018976	0.000159096 PTTG1 pituitary tumor-transforming 1
235080	0.000566403 PDGFRA platelet-derived growth factor receptor, alpha polypeptide
307255	1.71E-06 ICB-1 basement membrane-induced gene
154093	8.41E-06 CIR CBF1 interacting corepressor
138059	0.017914037 FLJ20374 hypothetical protein FLJ20374
363146	0.002345896 PPP3R1 protein phosphatase 3 (formerly 2B), regulatory subunit B (19kD), alpha isoform (calcineurin B, type I)
1704527	4.34E-05 BCRP2 Breakpoint cluster region protein, uterine leiomyoma, 2
150897	7.05E-06 B3GNT3 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3
504940	0.00048204 ESTs
267859	0.000661605 LOC51256 hypothetical protein
813280	0.000241441 ADSL adenylosuccinate lyase
1649746	0.039806156 ESTs
725076	0.002237924 NT5B 5'-nucleotidase (purine), cytosolic type B
236034	0.036288061 UCP2 uncoupling protein 2 (mitochondrial, proton carrier)
754509	0.000164308 MET met proto-oncogene (hepatocyte growth factor receptor)
31818	0.003705111 Homo sapiens clone 23700 mRNA sequence
220395	3.49E-09 FLJ23293 likely ortholog of mouse ADP-ribosylation-like factor 6 interacting protein 2
796759	0.03681114 VDAC3 voltage-dependent anion channel 3
768271	7.84E-07 Homo sapiens cDNA FLJ11436 fis, clone HEMBA1001213
951117	0.000316188 SHMT2 serine hydroxymethyltransferase 2 (mitochondrial)
731648	0.019893343 NFYA nuclear transcription factor Y, alpha
135811	2.09E-09 DEPP decidual protein induced by progesterone

1631711	0.000920277 EST
51063	0.002903498 ESTs
824001	0.003653268 FLJ10342 hypothetical protein FLJ10342
825740	0.043917654 DKFZP434J1813 DKFZp434J1813 protein
530761	0.007489303 ADSS adenylosuccinate synthase
266135	0.016029967 ESTs, Highly similar to S21424 nestin [H.sapiens]
1509540	0.003570072 HRH1 histamine receptor H1
796767	0.00038577 DKFZP564D0764 DKFZP564D0764 protein
344588	0.004877897 KLK5 kallikrein 5
155064	0.015807797 USP13 ubiquitin specific protease 13 (isopeptidase T-3)
592540	0.001362977 KRT5 keratin 5 (epidermolysis bullosa simplex, Dowling-Meara/Kobner/Weber-Cockayne types)
624867	0.000152832 FLJ20186 hypothetical protein FLJ20186
214131	0.00084937 NIT2 Nit protein 2
1854539	5.38E-06 SAM68 GAP-associated tyrosine phosphoprotein p62 (Sam68)
51078	8.56E-06 ESTs, Weakly similar to JC5314 CDC28/cdc2-like kinase associating arginine-serine cyclophilin [H.sapiens]
1659533	6.94E-09 MATN4 matrin 4
42258	0.008593378 ESTs, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens]
843398	0.042747042 BMP2 bone morphogenetic protein 2
32493	2.00E-05 ITGA6 integrin, alpha 6
1671299	0.000270513 HRK harakiri, BCL2-interacting protein (contains only BH3 domain)
757873	5.86E-06 CDK5R1 cyclin-dependent kinase 5, regulatory subunit 1 (p35)
770579	0.034946932 CLDN3 claudin 3
665384	1.40E-09 KIAA1609 KIAA1609 protein
877772	7.08E-10 MRAS muscle RAS oncogene homolog
813609	1.83E-05 MP1 metalloprotease 1 (pitrilsin family)
122739	0.005245158 FLJ21918 hypothetical protein FLJ21918
783681	0.024373058 UREB1 upstream regulatory element binding protein 1
289027	0.029539479 Homo sapiens cDNA FLJ31413 fis, clone NT2NE2000259, moderately similar to OOCYTE ZINC FINGER PROTEIN XLCOF6.1
52031	0.005871121 ESTs
243295	0.000174047 DKFZP434J154 DKFZP434J154 protein

376298	0.008888435 CGI-203 CGI-203 protein
770588	0.047831695 Homo sapiens TTF-1 interacting peptide 20 mRNA, partial cds
815214	7.86E-05 CH13L2 chitinase 3-like 2
2016632	0.028295772 ESTs, Moderately similar to T00359 hypothetical protein KIAA0680 [H.sapiens]
131563	4.01E-05 Homo sapiens cDNA FLJ13443 fis, clone PLACE1002853
254004	0.047241769 LOC51639 CGI-110 protein
814270	0.000160656 PMSCL1 polymyositis/scleroderma autoantigen 1 (75kD)
1468431	4.32E-05 LOC131601 seven transmembrane domain orphan receptor
783698	3.71E-07 LPIN1 lipin 1
504201	0.014811257 Homo sapiens, clone IMAGE:3677194, mRNA, partial cds
248531	4.67E-07 GMPS guanine monophosphate synthetase
108316	0.004877897 RAB3L1 RAB3A interacting protein (rab3)-like 1
200402	0.001715387 DJ616B8.3 hypothetical protein dj616B8.3
1610490	1.12E-05 CSNK1D casein kinase 1, delta
813629	0.001013874 YME1L1 YME1 (S.cerevisiae)-like 1
377252	5.60E-06 ADORA2B adenosine A2b receptor
49117	0.010535254 KIAA0215 KIAA0215 gene product
377253	0.003016551 FLJ14728 hypothetical protein FLJ14728
366830	0.006482896 ESTs
855872	0.035143688 NRD1 nardilysin (N-arginine dibasic convertase)
366834	0.021925399 EVPL envoplakin
1686314	3.96E-09 Homo sapiens cDNA FLJ31627 fis, clone NT2R12003338
755506	0.020241721 ANXA4 annexin A4
756163	0.003928565 BCR breakpoint cluster region
1642186	0.009231307 DPH2L2 diphtheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 2
1552374	0.000107772 PLSCR3 phospholipid scramblase 3
428163	0.04294858 ESTs, Weakly similar to NAH6_HUMAN SODIUM/HYDROGEN EXCHANGER 6 [H.sapiens]
1604220	0.000124487 LRPPRC leucine-rich PPR-motif containing
280907	0.001755052 LOC57209 Kruppel-type zinc finger protein
815235	0.000153521 RCD-8 autoantigen
1541958	0.001831779 POU2AF1 POU domain, class 2, associating factor 1
239724	0.000451254 Homo sapiens mRNA; cDNA DKFZp667B0711 (from clone DKFZp667B0711)

272748	0.001611957 D1S155E NRAS-related gene
1868626	0.033272185 PFKL phosphofructokinase, liver
814297	0.002489422 PEPD peptidase D
768619	0.016678558 Homo sapiens cDNA FLJ32643 fis, clone SYNOV2001212
950516	0.007644628 CNM4 cyclin M4
80549	0.02497657 PBX2 pre-B-cell leukemia transcription factor 2
51408	0.00712188 DSCR1L1 Down syndrome critical region gene 1-like 1
366848	3.47E-08 ESTs
825005	1.29E-05 IPLA2(GAMMA) intracellular membrane-associated calcium-independent phospholipase A2 gamma
739193	0.002561152 CRABP1 cellular retinoic acid-binding protein 1
301735	0.03966603 TGM3 transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)
358689	0.039496567 EPHB2 EphB2
2030301	0.017481981 SLIT3 slit (Drosophila) homolog 3
1550783	0.009173647 CHORDC1 cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1
824068	0.047848128 COX5A cytochrome c oxidase subunit Va
345586	0.003770645 TNFRSF12 tumor necrosis factor receptor superfamily, member 12 (translocating chain-association membrane protein)
813645	0.000248914 FLJ20500 hypothetical protein
741474	4.08E-06 GPI glucose phosphate isomerase
502625	0.000483976 FLJ21212 hypothetical protein FLJ21212
180263	0.005375632 KIAA0537 KIAA0537 gene product
377275	5.69E-15 TRIM29 tripartite motif-containing 29
127510-2	7.79E-05 CDC25A cell division cycle 25A
41650	0.044529607 HGF hepatocyte growth factor (heparocyte A; scatter factor)
2019214	0.00105118 CAD carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
281580	0.035143688 ESTs
842794	2.57E-05 KIAA1668 KIAA1668 protein
841057	1.17E-05 MAGE-E1 MAGE-E1 protein
530036	0.007079545 FLJ13078 hypothetical protein FLJ13078
813651	0.000139851 ALAS1 aminolevulinatase, delta-, synthase 1
2308314	0.016063781 KIAA1055 KIAA1055 protein
785616	0.005985046 SSR1 signal sequence receptor, alpha (translocon-associated protein alpha)

2604635	0.001601276 YAP1 Yes-associated protein 1, 65 kDa
50483	0.001534143 FBLN5 fibulin 5
1509904	0.020270563 PTGS2 prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)
809784	1.53E-05 KLK6 kallikrein 6 (neurosin, zyme)
725454	0.010208539 CKS2 CDC28 protein kinase 2
490649	3.45E-05 MCCC1 methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)
146605	0.012998471 FPR1 formyl peptide receptor-like 1
773183	9.02E-05 AF093680 similar to mouse Gli3 or D. melanogaster transcription factor IIB
845355	0.038531356 CTSC cathepsin C
1570339	1.02E-06 Homo sapiens, clone IMAGE:3948909, mRNA, partial cds
83120	0.000644819 RBM10 RNA binding motif protein 10
753946	0.001034397 HKE2 HLA class II region expressed gene KE2
744047	0.000853947 PLK polo (Drosophila)-like kinase
814617	0.001106068 MEF2A MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A)
813671	7.06E-05 ESTs, Weakly similar to T31636 hypothetical protein Y57A10A.n - Caenorhabditis elegans [C.elegans]
815276	0.038667897 NUP62 nucleoporin 62kD
813673	0.011252089 HDGF hepatoma-derived growth factor (high-mobility group protein 1-like)
2018297	0.038531356 CTL2 CTL2 gene
2009477	0.006324566 CD6 CD6 antigen
2713047	0.000148737 PVR poliovirus receptor
844703	7.67E-08 T-STAR Sam68-like phosphotyrosine protein, T-STAR
703541	1.21E-05 KIAA1858 KIAA1858 protein
2062028	0.001614105 ZNF259 zinc finger protein 259
770935	0.000827726 Th3 hypothetical protein FLJ13511
29927	0.012880496 FLJ10737 hypothetical protein FLJ10737
42627	0.035383143 COCH coagulation factor C (Limulus polyphemus homolog); cochlin
51448	0.00048184 ATF3 activating transcription factor 3
133518	0.000238959 MAPRE2 microtubule-associated protein, RPB/EB family, member 2
1455394	2.92E-06 HCS cytochrome c
1898758	0.011460543 BCE-1 BCE-1 protein
36393-2	0.005878639 ACAT2 acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)
815285	0.012980026 ERPROT213-21 protein with polyglutamine repeat; calcium (ca2+) homeostasis endoplasmic reticulum

	protein
486787	0.001271197 CNN3 calponin 3, acidic
626841	0.012861341 MET met proto-oncogene (hepatocyte growth factor receptor)
2308346	0.027141267 CDK2 cyclin-dependent kinase 2
756502	0.000554935 NUDT1 nudix (nucleoside diphosphate linked moiety X)-type motif 1
502669	9.98E-06 HDAC2 histone deacetylase 2
129644	0.003508671 SSH3BP1 spectrin SH3 domain binding protein 1
898328	6.78E-07 EDR2 early development regulator 2 (homolog of polyhomeotic 2)
756509	0.041594075 H105E3 NAD(P) dependent steroid dehydrogenase-like; H105e3
745003	0.002269285 ZNF76 zinc finger protein 76 (expressed in testis)
590242	0.000669517 ESTs
841091	0.000803586 FAF1 Fas (TNFRSF6) associated factor 1
841093	0.000742995 CUL1 cullin 1
345916	0.000621801 Homo sapiens mRNA; cDNA DKFZp564N1063 (from clone DKFZp564N1063)
1460224	0.006815479 ESTs. Weakly similar to I38133 protein kinase [H.sapiens]
379200	0.00041118 IRAK1 interleukin-1 receptor-associated kinase 1
2009491	0.005321091 LOC51191 cyclin-E binding protein 1
41698	0.00083009 PGFMC1 progesterone receptor membrane component 1
2306752	0.000328235 STMN2 stathmin-like 2
813698	0.009151254 SPRY2 sprouty (Drosophila) homolog 2
898332	0.001879562 NPR1 natriuretic peptide receptor A/guanylate cyclase A (atrial natriuretic peptide receptor A)
856887	0.02806084 ESTs
1570364	0.005587928 FLJ21324 hypothetical protein FLJ21324
950578	0.000159834 NDUFA5 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13)
745011	3.47E-05 KIAA1750 KIAA1750 protein
178324	0.04004725 ESTs
280970	0.00148396 NOL1 nucleolar protein 1 (120kD)
309161-2	0.001831364 TBX2 T-box 2
788205	0.001756144 SOX4 SRY (sex determining region Y)-box 4
755578	7.43E-08 SLC7A5 solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
786605	8.78E-05 APG-1 heat shock protein (hsp110 family)
123774	0.003147591 ESTs

83156	0.003569567 C6orf34 chromosome 6 open reading frame 34
416075	0.003099407 TCF19 transcription factor 19 (SC1)
773502	0.018979013 ESTs, Weakly similar to 365824 reverse transcriptase homolog [H.sapiens]
502682	0.037642103 ENIGMA enigma (LIM domain protein)
502689	0.029859423 Homo sapiens clone HH409 unknown mRNA
309288	0.005363273 RFC4 replication factor C (activator 1) 4 (37kD)
307687	0.000599469 PRSS16 protease, serine, 16 (thymus)
44255	6.27E-06 MRPL3 mitochondrial ribosomal protein L3
1926024	0.004189378 BCL2L12 BCL2-like 12 (proline rich)
1160723	2.20E-05 LIMK2 LIM domain kinase 2
85840	0.000112138 NNMT nicotinamide N-methyltransferase
130201	0.000950305 ICAM2 intercellular adhesion molecule 2
33837	0.004299371 KIAA1500 KIAA1500 protein
530093	0.000479617 MPZL1 myelin protein zero-like 1
1358393	0.0011328 MAP2K3 mitogen-activated protein kinase kinase 3
282587	0.000754806 CA11 carbonic anhydrase XI
502690	0.00352586 RPN1 ribophorin 1
626874	9.10E-08 FLJ23399 hypothetical protein FLJ23399
853562	0.023644346 TRIM28 tripartite motif-containing 28
782339	8.33E-05 PRKAB1 protein kinase, AMP-activated, beta 1 non-catalytic subunit
162308-2	0.000128308 CYR1 cysteine and tyrosine-rich protein 1
366126	2.91E-05 KIAA0354 KIAA0354 gene product
703581	0.034266941 PRG1 proteoglycan 1, secretory granule
741831	0.02005317 PLTP phospholipid transfer protein
825085	3.88E-07 ST14 suppression of tumorigenicity 14 (colon carcinoma, matrilysin, epithin)
814662	0.016952234 AP4B1 adaptor-related protein complex 4, beta 1 subunit
1468820	0.004338248 NOS3 nitric oxide synthase 3 (endothelial cell)
852913	0.033456546 SNRPF small nuclear ribonucleoprotein polypeptide F
704532	0.000420604 NMI1 N-myc (and STAT) interactor
245296	0.049442498 RAD52 RAD52 (S. cerevisiae) homolog
1880757	0.006991988 MAP3K5 mitogen-activated protein kinase kinase kinase 5
788234	4.76E-08 ID4 inhibitor of DNA binding 4, dominant negative helix-loop-helix protein

022041001010PC	
741841	0.003707205 DDX11 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase)
211216	0.024810654 KLF1 Kruppel-like factor 1 (erythroid)
360254	0.000831262 CYR61 cysteine-rich, angiogenic inducer, 61
741842	0.000446292 LOC51690 U6 snRNA-associated Sm-like protein LSM7
363597	0.000180473 C11orf8 chromosome 11 open reading frame 8
726464	0.001854106 SPAG9 sperm associated antigen 9
49502	0.0009273 CYLN2 cytoplasmic linker 2
47900	0.006683198 KIAA1382 amino acid transporter 2
529861	1.29E-05 PSMB6 proteasome (prosome, macropain) subunit, beta type, 6
810391	0.016029967 HYAL1 hyaluronoglucosaminidase 1
2322038	5.74E-07 COL4A6 collagen, type IV, alpha 6
2012757	0.000801869 D2S448 Melanoma associated gene
1632011	0.0039532 NPR2 natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)
845709	1.35E-05 ESTs
470393	1.08E-05 MMP7 matrix metalloproteinase 7 (matrilysin, uterine)
132911	0.001603821 PPP1CB protein phosphatase 1, catalytic subunit, beta isoform
756556	0.008247752 SERPING1 serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1
1635359	0.031634717 RASD1 RAS, dexamethasone-induced 1
753215	4.53E-06 GNAI1 guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1
738916	0.014632388 REV1L REV1 (yeast homolog)-like
361204	1.64E-06 COL9A3 collagen, type IX, alpha 3
1536727	0.022064191 MGC11324 hypothetical protein MGC11324
2096458	4.36E-08 CALU calumenin
869234	0.005357267 ESTs
739578	0.013280693 C4.4A GPI-anchored metastasis-associated protein homolog
788247	0.020732026 CUL2 cullin 2
430834	0.027276602 Homo sapiens, Similar to RIKEN cDNA 2810405F18 gene, clone MGC:22960 IMAGE:4865283, mRNA, complete cds
1639640	0.001388783 EIF5A eukaryotic translation initiation factor 5A
564492	2.90E-05 MTCN2 mitochondrial carrier homolog 2
244654	0.001763838 ELAC1 elac (E.coli) homolog 1
1574693	0.000601881 SLB selective LIM binding factor, rat homolog

860013	0.024373058 MGC1136 hypothetical protein MGC1136
897720	0.000629574 TRO trophinin
137862	0.028270162 HIP-55 src homology 3 domain-containing protein HIP-55
1635364	3.42E-06 LSM2 U6 snRNA-associated Sm-like protein
1551030	0.031216746 CDA cytidine deaminase
293328	0.000795582 C2orf2 chromosome 2 open reading frame 2
1404396	0.000304786 PLCB3 phospholipase C, beta 3 (phosphatidylinositol-specific)
292388	0.004770631 LOC55977 hypothetical protein 24636
840493	0.006951821 RNASE1 ribonuclease, RNase A family, 1 (pancreatic)
268188	0.000728707 PRRG1 proline-rich Gla (G-carboxyglutamic acid) polypeptide 1
503671	2.23E-08 Homo sapiens cDNA FLJ14368 fts, clone HEMBA1001122
645495	0.014557615 BICD1 Bicaudal D (Drosophila) homolog 1
80946	0.005577147 ABCE1 ATP-binding cassette, sub-family E (OABP), member 1
1883327	0.015005389 Homo sapiens cDNA FLJ30999 fts, clone HLUNG1000110, weakly similar to PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR
897731	0.014470496 KIAA0786 latrophilin
897732	5.30E-05 SAD1 SnRNP assembly defective 1 homolog
1950274	0.025668592 ESTs
753236	0.000420604 ESTs, Weakly similar to S71512 hypothetical protein T2 - mouse [M.musculus]
1055581	0.038751321 DKFZP564K192 likely ortholog of mouse dysbindin
344243	0.00041118 UMPK uridine monophosphate kinase
788264	0.023178776 DPAGT1 dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)
774502	0.031310371 PTPN12 protein tyrosine phosphatase, non-receptor type 12
49532	8.13E-08 VIM vimentin
1558675	2.00E-07 SOX10 SRY (sex determining region Y)-box 10
308682	0.000155359 ABCF2 ATP-binding cassette, sub-family F (GCN20), member 2
773564	0.000739744 NIN283 nerve injury gene 283
2719303	0.015247808 SLC18A1 solute carrier family 18 (vesicular monoamine), member 1
125722	0.003691973 DGUOK deoxyguanosine kinase
509570	0.015704565 Homo sapiens cDNA: FLJ22656 fts, clone HSI07655
231574	0.048699543 FB11 HIV-1 inducer of short transcripts binding protein; lymphoma related factor

022041001010PC	
301061	0.000176121 COL18A1 collagen, type XVIII, alpha 1
79629	0.011251927 CXCR4 chemokine (C-X-C motif), receptor 4 (fusin)
344251	0.012443564 FLJ10783 hypothetical protein FLJ10783
795499	0.010004815 NDRG4 NDRG family, member 4
772912	0.02555164 AGS3 likely ortholog of rat activator of G-protein signaling 3
156473	0.001838545 EPHX2 epoxide hydrolase 2, cytoplasmic
772913	1.23E-11 Homo sapiens cDNA FLJ31951 fis, clone NT2RP7007177, weakly similar to Homo sapiens multiple membrane spanning receptor TRC8 mRNA
773571	2.09E-06 GTF3C3 general transcription factor III C, polypeptide 3 (102kD)
630013	0.000293426 MSH2 mutS (E. coli) homolog 2 (colon cancer, nonpolyposis type 1)
856167	8.78E-05 TARS threonyl-tRNA synthetase
2322079	0.020096884 EST
1472754	0.019822944 COX6B cytochrome c oxidase subunit VIb
756595	6.16E-05 S100A10 S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))
50884	0.002936718 DYRK2 dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
509589	0.00458557 LOC51122 HSPC042 protein
884657	0.036349025 TIMM8B translocase of inner mitochondrial membrane 8 (yeast) homolog B
121454	0.004821899 ALOX12 arachidonate 12-lipoxygenase
112636	1.36E-05 IL1RAP interleukin 1 receptor accessory protein
2062415	1.01E-05 GMD5 GDP-mannose 4,6-dehydratase
135503	0.022046067 BRD4 bromodomain-containing 4
2062418	0.034945258 AIM1 absent in melanoma 1
843070	4.81E-05 NUP88 nucleoporin 88kD
1759582	0.000276452 FN14 type I transmembrane protein Fn14
50892	0.044429786 Homo sapiens, clone MGC:9913 IMAGE:3870821, mRNA, complete cds
566421	0.023116508 PIMT PRIP-interacting protein with methyltransferase domain
841478	0.000244327 VIT1 vitiligo-associated protein VIT-1
1860497	0.000102553 Homo sapiens, clone MGC:5352 IMAGE:3048106, mRNA, complete cds
418049	1.52E-06 Homo sapiens cDNA: FLJ21909 fis, clone HEP03834
855521	0.040241164 KRT18 keratin 18
767312	0.040844999 PLD2 phospholipase D2
235882	0.001352198 KIAA0709 endocytic receptor (macrophage mannose receptor family)

306318	3.49E-06 ORC6L origin recognition complex, subunit 6 (yeast homolog)-like
71087	0.022618851 MAFK v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein F
840821	0.044848397 SSR4 signal sequence receptor, delta (translocan-associated protein delta)
525926	6.55E-07 SDC1 syndecan 1
1686766	9.44E-06 RAGD Rag D protein
613056	0.005068207 RCN1 reticulocalbin 1, EF-hand calcium binding domain
79655	0.003417271 MGC2722 hypothetical protein MGC2722
489729	1.40E-07 ETS1 v-ets avian erythroblastosis virus E26 oncogene homolog 1
2610539	0.005368978 KRT6B keratin 6B
795805	0.001440423 KIAA0332 KIAA0332 protein
841485	0.01354434 Homo sapiens cDNA FLJ31058 fis, clone HSYRA2000828
74713	0.00017506 FLJ20059 hypothetical protein FLJ20059
753278	1.39E-05 CXCL16 chemokine (C-X-C motif) ligand 16
796469	0.016508823 HSPC150 HSPC150 protein similar to ubiquitin-conjugating enzyme
1613496	0.001928041 EST
430894	0.012480222 TLN1 talin 1
1947381	0.000752302 FLJ22329 hypothetical protein FLJ22329
2499237	0.000760968 SERPINB5 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5
321708	0.01621547 TFDP1 transcription factor Dp-1
843091	0.000367291 MGC20533 similar to RIKEN cDNA 2410004L22 gene (M. musculus)
588368	0.01394813 KIAA0947 KIAA0947 protein
590640	7.53E-05 PDXK pyridoxal (pyridoxine, vitamin B6) kinase
1519013	1.16E-06 Homo sapiens, clone IMAGE:3537447, mRNA, partial cds
823850	0.001603821 RAI14 retinoic acid induced 14
357396	0.038563775 Homo sapiens cDNA: FLJ23137 fis, clone LNG08842
345234	0.002720745 ESTs, Weakly similar to T00705 N-chimerin homolog F25965_3 [H.sapiens]
753285	0.047573891 GYG glycogenin
566443	6.48E-06 Homo sapiens cDNA FLJ12793 fis, clone NT2RP2002033
796475	2.49E-07 FHL3 four and a half LIM domains 3
83549	0.000116498 C1R complement component 1, r subcomponent
1637311	0.003072498 KIAA0036 KIAA0036 gene product
810753	0.000438842 MRPS10 mitochondrial ribosomal protein S10

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41300	8.52E-05 Homo sapiens clones 24714 and 24715 mRNA sequence
1554727	0.005687928 HSF2 heat shock transcription factor 2
743810	0.012831119 MGC2577 hypothetical protein MGC2577
140071	0.011056053 FRZB fizzled-related protein
726830	0.022786019 FLJ10748 hypothetical protein FLJ10748
282977	0.039374425 ADCY2 adenylate cyclase 2 (brain)
884690	0.001462177 CCT8 chaperonin containing TCP1, subunit 8 (theta)
282978	0.000356685 TGFBR2 transforming growth factor, beta 2
823864	0.005015434 TCN2 transcobalamin II; macrocytic anemia
415814	0.000792587 LOC56901 NADH:ubiquinone oxidoreductase MLRQ subunit homolog
511107	0.005854823 CCT4 chaperonin containing TCP1, subunit 4 (delta)
741139	0.000808096 EYAA2 eyes absent (Drosophila) homolog 2
323322	0.008351255 ESTs
810762	0.018133375 YKT6 SNARE protein
49595	0.010562779 DKFZP434F091 DKFZP434F091 protein
1637328	0.000165971 AOX1 aldehyde oxidase 1
2062453	0.001470365 DKFZP727G051 DKFZP727G051 protein
703972	0.002002869 KIAA0699 KIAA0699 protein
669375	6.11E-06 DKK1 dickkopf (Xenopus laevis) homolog 1
489755	0.001048773 ADAM12 a disintegrin and metalloproteinase domain 12 (meltrin alpha)
611481	1.40E-06 TCF-3 HMG-box transcription factor TCF-3
487071	0.000245994 GNRH1 gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)
417424	0.000622484 ABP/ZF Alu-binding protein with zinc finger domain
788617	9.28E-09 LOC91689 hypothetical gene supported by AL449243
825478	0.010722629 ZNF146 zinc finger protein 146
431869	0.017680318 Homo sapiens, clone IMAGE:3506202, mRNA, partial cds
897011	0.00140216 KIAA0842 KIAA0842 protein
1910785	0.001443649 ATP11A ATPase, Class VI, type 11A
813609-2	5.33E-06 MP1 metalloprotease 1 (pitrilysin family)
284592	5.11E-11 DKFZp762A227 hypothetical protein DKFZp762A227
788620	4.20E-05 Homo sapiens, clone MGC:17225 IMAGE:4151716, mRNA, complete cds
1837280	0.002741302 EST

504940-2	6.84E-05 ESTs
795841	0.000205324 FLJ14466 hypothetical protein FLJ14466
345262	0.032131824 PCDHB2 protocadherin beta 2
162308	0.000536545 CYRR1 cysteine and tyrosine-rich protein 1
853977	0.000294844 ESTs
1534430	0.012397017 GUCY1B2 guanylate cyclase 1, soluble, beta 2
450464	0.008351255 ACVR2 activin A receptor, type II
142788	4.92E-08 SERPINH2 serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 2
486436	0.002295943 UGP2 UDP-glucose pyrophosphorylase 2
629839	0.034919482 dJ908M14.2 hypothetical protein dJ908M14.2
781014	2.92E-05 ST5 suppression of tumorigenicity 5
241705	0.002362784 PYGL phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)
782756	1.92E-05 TBP1 TBP-like 1
293715	0.047831695 RAB1 RAB1, member RAS oncogene family
2345302	0.027994066 KIAA0675 KIAA0675 gene product
509943	0.000400309 DKC1 dyskeratosis congenita 1, dyskerin
1534440	0.033905314 EST
743851	0.024878213 ESTs, Weakly similar to S55916 ribosomal protein S5, cytosolic [H.sapiens]
1456799	0.019816713 Homo sapiens cDNA FLJ32537 fis, clone SMINT2000400, highly similar to Homo sapiens FRG1 mRNA
415851	6.35E-08 ARHE ras homolog gene family, member E
248256	2.71E-07 KIAA1691 KIAA1691 protein
810002	3.90E-05 Homo sapiens, clone M3C.19762 IMAGE:3636045, mRNA, complete cds
626502	4.10E-08 ARPC1B actin related protein 2/3 complex, subunit 1B (41 kD)
167268	0.047573891 ESTs
781026	0.016470796 Homo sapiens cDNA FLJ11801 fis, clone HEMBA1006253, weakly similar to DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR
462926	0.01888892 NEK2 NIMA (never in mitosis gene a)-related kinase 2
156270-2	0.004049154 ESTs
44692	0.000993361 CRHR1 corticotropin releasing hormone receptor 1
753625	0.00994019 Homo sapiens cDNA FLJ14844 fis, clone PLACE1000133, highly similar to TRANSCRIPTION FACTOR BTF3
683059	2.83E-06 CEP3 Cdc42 effector protein 3

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756968	0.015062537 EFNB1 ephrin-B1
1898426	0.02483948 MGC4268 hypothetical protein MGC4268
739983	0.0041899 KIAA0042 KIAA0042 gene product
1473788	0.016370991 TRADD TNFRSF1A-associated via death domain
66902	0.000352001 Homo sapiens cDNA FLJ32121 fis, clone PEBLM1000083
41358	0.037052367 MEIS2 Meis (mouse) homolog 2
743866	2.59E-07 FLJ10201 hypothetical protein FLJ10201
725143	0.040000458 FLJ22418 hypothetical protein FLJ22418
49920	0.035411663 PTDSS1 phosphatidylserine synthase 1
260303	4.78E-05 ETS2 v-ets avian erythroblastosis virus E26 oncogene homolog 2
343695	0.002155839 Homo sapiens cDNA FLJ31668 fis, clone NT2RI2004916
713782	0.000328235 ADAM15 a disintegrin and metalloproteinase domain 15 (metargidin)
240780	0.000237546 NINJ2 ninjurin 2
136534	0.003770645 MGC10753 hypothetical protein MGC10753
462939	0.036642651 Homo sapiens cDNA FLJ31303 fis, clone LIVER1000082
291057	0.024002401 CDKN2C cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
417473	0.010898808 GNAS1 guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1
725152	3.29E-10 DKFZp762A227 hypothetical protein DKFZp762A227
814309	0.031933058 PIST PDZ/coiled-coil domain binding partner for the rho-family GTPase TC10
858153	2.72E-07 NFIL3 nuclear factor, interleukin 3 regulated
772220	7.74E-06 PDIR for protein disulfide isomerase-related
2057973	0.043575209 CCND3 cyclin D3
781047	0.000900648 BUB1 budding uninhibited by benzimidazoles 1 (yeast homolog)
37491	0.000305556 TRIP10 thyroid hormone receptor interactor 10
134942	0.011506861 FBXL11 f-box and leucine-rich repeat protein 11
1553054	0.013614879 PRSS12 protease, serine, 12 (neutrypsin, motolysin)
208718	1.94E-09 ANXA1 annexin A1
230235	0.018133375 CRFG G protein-binding protein CRFG
214990	1.04E-07 GSN gelsolin (amyloidosis, Finnish type)
418422	9.66E-07 PPBP pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2)
123441	0.02798739 GALNT2 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2

	(GalNAc-T2)
742143	0.03760007 CD5 CD5 antigen (p58-62)
69184	0.000101368 SUD sucd (suppressor of bimD6, Aspergillus nidulans) homolog
795893	0.010292994 PPP1R15A protein phosphatase 1, regulatory (inhibitor) subunit 15A
120106	0.018649252 CASP1 caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)
2919651	0.000222692 PGL YRP peptidoglycan recognition protein
898010	0.000371143 EST
858167	8.01E-05 FACL4 fatty-acid-Coenzyme A ligase, long-chain 4
782794	0.001204679 SLC25A19 solute carrier family 25 (mitochondrial deoxynucleotide carrier), member 19
33500	2.81E-08 Homo sapiens clone 23556 mRNA sequence
133213	0.001335593 FUT4 fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
1553065	0.010881395 FLJ14993 hypothetical protein FLJ14993
416833	0.016095957 FKBP5 FK506-binding protein 5
68534	0.006753838 Homo sapiens cDNA: FLJ22290 fis, clone HRC04405
1574330	7.62E-05 GROS1 growth suppressor 1
502367	0.027654372 FBLN1 fibulin 1
502369	3.35E-06 PDGCD5 programmed cell death 5
856575	6.13E-05 APP amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)
366591	3.53E-05 TIAM2 T-cell lymphoma invasion and metastasis 2
290422	2.17E-06 ZNF216 zinc finger protein 216
1534493	1.17E-07 ESTs
280666	0.011314426 SEMA4D sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D
344672	0.017131408 DKFZp761J139 hypothetical protein DKFZp761J139
23758	0.005068225 Homo sapiens clone 23758 mRNA sequence
858183	0.001057603 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 684990
629896	0.000370779 MAP1B microtubule-associated protein 1B
725188	0.027824136 MDH1 malate dehydrogenase 1, NAD (soluble)
858188	0.042931319 Homo sapiens cDNA FLJ32144 fis, clone PLACE5000105, highly similar to Mus musculus mRNA for heparan sulfate 6-sulfotransferase 2
810057	6.03E-08 CSDA cold shock domain protein A
2062825	0.001409555 KIAA0964 KIAA0964 protein

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50506	0.000975654 MAFK6 mitogen-activated protein kinase 6
739235	0.000209372 STK25 serine/threonine kinase 25 (Ste20, yeast homolog)
345621	0.002744036 CXX1 CAAAX box 1
743113	1.29E-05 KLIK13 kalikrein 13
133236	4.10E-05 RBMX RNA binding motif protein, X chromosome
814341	0.004173726 DAP1 dual adaptor of phosphotyrosine and 3-phosphoinositides
2391494	0.000271971 EFNA4 ephrin-A4
772261	0.028380323 MAFK14 mitogen-activated protein kinase 14
704216	2.82E-05 MAF4K2 mitogen-activating protein kinase kinase kinase 2
293785	0.000141314 ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]
770665	0.000828447 FLJ12750 hypothetical protein FLJ12750
264640	0.010224986 CLTB clathrin, light polypeptide (Lcb)
824117	0.01125807 VRK2 vaccinia related kinase 2
1711877	0.01333655 ESTs
503335	0.002578724 FLJ11196 hypothetical protein FLJ11196
811013	0.001613372 AMPD2 adenosine monophosphate deaminase 2 (isoform L)
1475730	0.015717591 CCT6A chaperonin containing TCP1, subunit 6A (zeta 1)
52120	4.80E-07 DTX1 deltex (Drosophila) homolog 1
2013094	0.003571882 KIF1C kinesin family member 1C
768393	0.001209009 FLJ10829 hypothetical protein FLJ10829
128711	7.44E-05 ANLN anilin (Drosophila Scraps homolog), actin binding protein
1635032	0.002192122 NOLA1 nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)
137535	0.003910158 TIF1 transcriptional intermediary factor 1
1870684	0.020116819 PCYT1A phosphate cytidylyltransferase 1, choline, alpha isoform
825861	0.047376087 NUP153 nucleoporin 153KD
809824	0.000141145 TMEPA1 transmembrane, prostate androgen induced RNA
815303	0.002677229 DARS aspartyl-tRNA synthetase
842849	0.002998058 POLA2 polymerase (DNA-directed), alpha (70KD)
22040	0.004853144 MMP9 matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase)
24729	4.25E-06 CHRM1 cholinergic receptor, muscarinic 1
159462	9.93E-07 MSE5 serum constituent protein
811020	1.65E-11 Homo sapiens, clone IMAGE:4278205, mRNA, partial cds

2307420	0.040870882 TUBB tubulin, beta polypeptide
627521	0.014104273 ESTs, Weakly similar to KIAA1140 protein [H.sapiens]
361688	0.023373299 DPP6 dipeptidylpeptidase VI
1603358	0.019799335 FAT FAT tumor suppressor (Drosophila) homolog
1946069	6.72E-08 SPHK1 sphingosine kinase 1
268946	0.000809644 Homo sapiens cDNA FLJ31861 fis, clone NT2RP7001319
824132	0.00066839 Homo sapiens, Similar to cofactor required for Sp1 transcriptional activation, subunit 8 (34KD), clone MGC:11274 IMAGE:3944264, mRNA, complete cds
266263	0.012980026 ESTs
1710152	0.041184366 SOAT1 sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1
813714	0.000195754 CFLAR CASP8 and FADD-like apoptosis regulator
813719	0.000693345 ESTs, Weakly similar to DAP1_HUMAN DEATH-ASSOCIATED PROTEIN 1 [H.sapiens]
712401	0.005587928 PIK3CD phosphoinositide-3-kinase, catalytic, delta polypeptide
785392	0.036628745 DKFZP434F2021 DKFZP434F2021 protein
1883008	0.008613382 EST, Weakly similar to T24581 hypothetical protein T06D8.8 - Caenorhabditis elegans [C.elegans]
1637732	5.51E-05 PPAN peter pan (Drosophila) homolog
1493390	4.71E-06 ILF2 interleukin enhancer binding factor 2, 45kD
595213	0.027525584 BM-009 hypothetical protein
842861	0.018460389 HNRPR heterogeneous nuclear ribonucleoprotein R
878833	1.99E-05 UCHL1 ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
1631853	0.000227064 Homo sapiens, Similar to RIKEN cDNA 2410003K15 gene, clone MGC:20424 IMAGE:4646294, mRNA, complete cds
132619	0.003085822 ESTs
502701	1.67E-08 FREQ frequenin (Drosophila) homolog
504308	3.20E-05 FLJ10540 hypothetical protein FLJ10540
950600	2.03E-06 Homo sapiens mRNA; cDNA DKFZp586C1019 (from clone DKFZp586C1019)
80633	0.001826411 TLR2 toll-like receptor 2
784744	0.001112368 MPKPHSH6 M-phase phosphoprotein 6
811044	1.63E-08 EST
845419	5.05E-05 FANCA Fanconi anemia, complementation group A
897427	0.018369144 Homo sapiens, clone IMAGE:3638994, mRNA, partial cds
878846	9.96E-12 BR13 brain protein 13

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345670	2.09E-06	NFYC nuclear transcription factor Y, gamma
1631868	0.038386276	MGC13061 hypothetical protein MGC13061
811054	0.019642843	GNA12 guanine nucleotide binding protein (G protein) alpha 12
839941	1.31E-05	FLJ14590 hypothetical protein FLJ14590
589751	0.000104128	HTATIP2 HIV-1 Tat interactive protein 2, 30 kDa
208001	0.000566004	CD59 CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)
1637756	0.000324573	ENO1 enolase 1, (alpha)
755612	9.22E-06	GPR39 G protein-coupled receptor 39
685045	0.002900139	ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]
306771	1.68E-06	TMSNB thymosin, beta, identified in neuroblastoma cells
377368	0.001270033	LOC57099 cell death regulator aven
898092	2.20E-05	CTGF connective tissue growth factor
1631874	0.020656474	LOC51068 CGI-07 protein
841149	0.004225448	TGFBR2 transforming growth factor, beta receptor II (70-80kD)
813742	6.19E-07	PTK7 PTK7 protein tyrosine kinase 7
785707	0.001862647	PRC1 protein regulator of cytokinesis 1

Table 3. Genes that are overexpressed in ER positive cells, and underexpressed in ER negative cells

GeneID	P-value	Description
AW473119	p < 1e-07	ESR1 estrogen receptor 1
AF088867	p < 1e-07	AGR2 anterior gradient 2 homolog (Xenopus laevis)
AW015443	p < 1e-07	ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
AW137092	p < 1e-07	Homo sapiens cDNA FLJ10561 fis, clone NT2RP2002672
BC017859	p < 1e-07	TFF3 trefoil factor 3 (intestinal)
AL137566	p < 1e-07	Homo sapiens mRNA, cDNA DKFZp586G0321 (from clone DKFZp586G0321)
NM_004496	p < 1e-07	HNF3A hepatocyte nuclear factor 3, alpha
AW451986	p < 1e-07	ESTs

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AW207206	p < 1e-07	ESTS	
AA412108	p < 1e-07	ESTS	
NM_001218	p < 1e-07	CA12 carbonic anhydrase XII	
AI128582	p < 1e-07	ESTS	
R41823	p < 1e-07	ESTS	
AF356492	p < 1e-07	DACH dachshund homolog (Drosophila)	
BC014962	p < 1e-07	GFRA1 GDNF family receptor alpha 1	
AA688021	p < 1e-07	ESTS	
AI200852	p < 1e-07	ESTS	
AW086163	p < 1e-07	ESTS	
AF007153	p < 1e-07	Homo sapiens clone 23736 mRNA sequence	
AI050855	p < 1e-07	ESTS	
AA569340	p < 1e-07	CYP2B7 cytochrome P450, subfamily 11B (phenobarbital-inducible), polypeptide 7	
AI125908	p < 1e-07	Homo sapiens cDNA FLJ30555 fis, clone BRAWH2003818	
BC013732	p < 1e-07	NAT1 N-acetyltransferase 1 (arylamine N-acetyltransferase)	
AA542898	p < 1e-07	P28 dynein, axonemal, light intermediate polypeptide	
AI820662	p < 1e-07	ESTS	
AA846824	p < 1e-07	ESTS	
NM_020974	p < 1e-07	CEGP1 CEGP1 protein	
AI373462	p < 1e-07	ESTS	
AJ009985	p < 1e-07	ANXA9 annexin A9	
BF433570	p < 1e-07	ESTS	
AI377320	p < 1e-07	ESTS	
NM_000767	p < 1e-07	CYP2B6 cytochrome P450, subfamily 11B (phenobarbital-inducible), polypeptide 6	
AF070632	p < 1e-07	Homo sapiens clone 24405 mRNA sequence	
AF131785	p < 1e-07	KIAA0882 KIAA0882 protein	
AW300348	p < 1e-07	Homo sapiens ovarian cancer-related protein 2 (OCR2) mRNA, complete cds	
AL512749	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp667D095 (from clone DKFZp667D095)	
AI733682	p < 1e-07	ESTS	
AW780011	p < 1e-07	ESTS	
AW135648	p < 1e-07	ESTS	
AI263695	p < 1e-07	NME5 non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	
NM_000044	p < 1e-07	AR androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)	

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AK000158	p < 1e-07	FLJ20151 hypothetical protein FLJ20151
AF176012	p < 1e-07	JDP1 J domain containing protein 1
BC018035	p < 1e-07	Homo sapiens, clone IMAGE:4819956, mRNA, partial cds
BC008429	p < 1e-07	C20orf14 chromosome 20 open reading frame 114
BF436400	p < 1e-07	EST
BC006496	p < 1e-07	PDZK1 PDZ domain containing 1
BC014659	p < 1e-07	NG22 NG22 protein
AA182477	p < 1e-07	ESTs
AI272823	p < 1e-07	ESTs
BC010951	p < 1e-07	PIP prolactin-induced protein
BC014948	p < 1e-07	MLPH melanophilin
AI026825	p < 1e-07	DNL2B dynein light chain 2B
BC015338	p < 1e-07	CPB1 carboxypeptidase B1 (tissue)
AI355477	p < 1e-07	ESTs
R60583	p < 1e-07	NOVA1 neuro-oncological ventral antigen 1
AK058158	p < 1e-07	Homo sapiens cDNA FLJ25429 fis, clone TST05630
		Homo sapiens, Similar to RIKEN cDNA 1700017111 gene, clone MGC:26847 IMAGE:4821517, mRNA, complete cds
BC014601	p < 1e-07	Homo sapiens cDNA FLJ14142 fis, clone MAMMA1002880
AK024204	p < 1e-07	KIAA0575 KIAA0575 gene product
AI874215	p < 1e-07	CAPN13 calpain 13
AK027176	p < 1e-07	SERPINA5 serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 5
BC008915	p < 1e-07	CYP4B1 cytochrome P450, subfamily IVB, polypeptide 1
BC017758	p < 1e-07	HS250839 gene for serine/threonine protein kinase
AI871614	p < 1e-07	RET ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)
AA903339	p < 1e-07	EST
AA553710	p < 1e-07	Homo sapiens, clone MGC:17393 IMAGE:3914851, mRNA, complete cds
BC016861	p < 1e-07	DKFZP4341092 DKFZP4341092 protein
AY009106	p < 1e-07	Homo sapiens, clone IMAGE:3899073, mRNA, partial cds
BC013438	p < 1e-07	HMGCS2 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)
NM_005518	p < 1e-07	Homo sapiens, clone MGC:5522 IMAGE:3454199, mRNA, complete cds
AW024203	p < 1e-07	Homo sapiens mRNA; cDNA DKFZP434E2321 (from clone DKFZp434E2321); partial cds
AL133619	p < 1e-07	FBP1 fructose-1,6-bisphosphatase 1
NM_000507	p < 1e-07	NPD009 NPD009 protein
AF237813	p < 1e-07	

AI828071	p < 1e-07	BCAS1 breast carcinoma amplified sequence 1
AA557177	p < 1e-07	EST
Z11162	p < 1e-07	AGTR1 angiotensin receptor 1
NM_007050	p < 1e-07	PTPR protein tyrosine phosphatase, receptor type, T
NM_007293	p < 1e-07	C4A complement component 4A
AK021931	p < 1e-07	Homo sapiens cDNA FLJ11869 fis, clone HEMBA1007002
AA130089	p < 1e-07	ESTs
BC007997	p < 1e-07	RERG RAS-like, estrogen-regulated, growth-inhibitor
AK055698	p < 1e-07	Homo sapiens cDNA FLJ31136 fis, clone IMR322001029
AI668602	p < 1e-07	ESTs, Weakly similar to JX0331 laurate omega-hydroxylase [H.sapiens]
AW261844	p < 1e-07	ESTs
AI337740	p < 1e-07	FLJ12650 hypothetical protein FLJ12650
AW073282	p < 1e-07	ESTs
BC000558	p < 1e-07	MAPT microtubule-associated protein tau
AI498298	p < 1e-07	FACVL1 fatty-acid-Coenzyme A ligase, very long-chain 1
AI570494	p < 1e-07	ESTs
AF209930	p < 1e-07	CHRD chordin
AK026756	p < 1e-07	KIAA1603 KIAA1603 protein
AW070592	p < 1e-07	ESTs
BC014189	p < 1e-07	MGC20702 hypothetical protein MGC20702
AL117406	p < 1e-07	ABCC11 ATP-binding cassette, sub-family C (CFTR/MRP), member 11
AI190693	p < 1e-07	ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]
NM_003561	p < 1e-07	PLA2G10 phospholipase A2, group X
AA513718	p < 1e-07	ESTs
BF591743	p < 1e-07	LPHB lipophilin B (uteroglobin family member), prostatein-like
AK026958	p < 1e-07	FLJ23305 hypothetical protein FLJ23305
AW016378	p < 1e-07	ESTs
BC017701	p < 1e-07	AD036 AD036 protein
AW294316	p < 1e-07	ESTs
BC006793	p < 1e-07	GATA3 GATA binding protein 3
AK026427	p < 1e-07	FLJ22774 hypothetical protein FLJ22774
NM_004310	p < 1e-07	ARH1 ras homolog gene family, member H
AK000181	p < 1e-07	FLJ20174 hypothetical protein FLJ20174
NM_016613	p < 1e-07	LOC51313 AD021 protein

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BC0000088	p < 1e-07	GSTM3 glutathione S-transferase M3 (brain)
BC011721	p < 1e-07	TUBA2 tubulin, alpha 2
AI631708	p < 1e-07	ESTs, Weakly similar to i312318A cystatin SA [H.sapiens]
NM_001756	p < 1e-07	SERPINA6 serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6
NM_004525	p < 1e-07	LRP2 low density lipoprotein-related protein 2
BC012613	p < 1e-07	CPA3 carboxypeptidase A3 (mast cell)
BC011348	p < 1e-07	FLJ12910 hypothetical protein FLJ12910
NM_001502	p < 1e-07	GP2 glycoprotein 2 (zymogen granule membrane)
AA807457	p < 1e-07	MYB v-myb myeloblastosis viral oncogene homolog (avian)
AL157505	p < 1e-07	Homo sapiens mRNA: cDNA DKFZp586P1124 (from clone DKFZp586P1124)
NM_005080	p < 1e-07	XBP1 X-box binding protein 1
AI277016	p < 1e-07	ESTs
AA648777	p < 1e-07	MS4A7 membrane-spanning 4-domains, subfamily A, member 7
AL360204	p < 1e-07	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 980547
BE967259	p < 1e-07	BCL2 B-cell CLL/lymphoma 2
BC012372	p < 1e-07	C4B complement component 4B
AI797041	p < 1e-07	TRH thyrotropin-releasing hormone
AI804588	p < 1e-07	BLU Elu protein
AI309080	p < 1e-07	ESTs
BT725007	p < 1e-07	ADRA2A adrenergic, alpha-2A-, receptor
AI253198	p < 1e-07	Homo sapiens cDNA FLJ13945 fis, clone Y79AA1000969
AK000373	p < 1e-07	FLJ20366 hypothetical protein FLJ20366
AI028773	p < 1e-07	ACOX2 acyl-Coenzyme A oxidase 2, branched chain
AW664923	0.000002	GRIA2 glutamate receptor, ionotropic, AMPA 2
BC004518	p < 1e-07	LOC51760 B/K protein
NM_002145	p < 1e-07	HOXB2 homeo box B2
NM_000792	p < 1e-07	DIO1 deiodinase, iodothyronine, type I
AK024872	p < 1e-07	SYTL2 synaptotagmin-like 2
BC015628	p < 1e-07	ABAT 4-aminobutyrate aminotransferase
BC000658	p < 1e-07	STC2 stannocalcin 2
AL050227	p < 1e-07	Homo sapiens mRNA: cDNA DKFZp586M0723 (from clone DKFZp586M0723)
AK027006	p < 1e-07	TNRC9 trinucleotide repeat containing 9
AA659816	p < 1e-07	ESTs
AA845338	p < 1e-07	FMO5 flavin containing monooxygenase 5

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BC012625	p < 1e-07	PPP1R3C protein phosphatase 1, regulatory (inhibitor) subunit 3C
AW015140	p < 1e-07	ESTs
AI992108	p < 1e-07	Homo sapiens cDNA FLJ25333 fis, clone TST00656
R39691	p < 1e-07	SYT1 synaptotagmin 1
BC001665	p < 1e-07	Homo sapiens, Similar to KIAA0843 protein, clone MGC:1835 IMAGE:2988043, mRNA, complete cds
AF403428	p < 1e-07	LRG leucine-rich alpha-2-glycoprotein
AK057315	p < 1e-07	TSGA2 testes specific A2 homolog (mouse)
R40824	p < 1e-07	FBXL7 F-box and leucine-rich repeat protein 7
AI732534	p < 1e-07	MBL1 mammaglobin 1
BC012375	p < 1e-07	KIAA1001 KIAA1001 protein
AI587351	0.0000012	CEACAM6 carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)
BC007681	p < 1e-07	RAB26 RAB26, member RAS oncogene family
AI694966	p < 1e-07	RAI2 retinoic acid induced 2
AL136926	p < 1e-07	DKFZP586M1120 hypothetical protein DKFZp586M1120
AW070746	p < 1e-07	NCAM2 neural cell adhesion molecule 2
AI432856	p < 1e-07	EST
AF384856	p < 1e-07	PGLYRP peptidoglycan recognition protein L precursor
AI823785	p < 1e-07	BC008967 hypothetical gene BC008967
BC014250	p < 1e-07	CHST8 carbohydrate (N)-acetylgalactosamine 4-O) sulfotransferase 8
R49089	p < 1e-07	ESTs, Moderately similar to T12539 hypothetical protein DKFZp434J154.1 [H.sapiens]
AW134740	p < 1e-07	DCAMKL1 doublecortin and Cam kinase-like 1
AL390084	p < 1e-07	LOC56964 hypothetical protein from EUROIMAGE 384293
AI056882	p < 1e-07	KIAA1493 KIAA1493 protein
AK000532	p < 1e-07	Homo sapiens cDNA FLJ20525 fis, clone KAT10610
N22687	p < 1e-07	ESTs
NM_003770	p < 1e-07	KRTHA7 keratin, hair, acidic, 7
AK000563	p < 1e-07	HRASLS2 HRAS-like suppressor 2
		Homo sapiens cDNA FLJ33105 fis, clone TRACH2000926, weakly similar to PROBABLE OXIDOREDUCTASE
AW082090	0.0000001	EPHD (EC 1.-.-.-)
AA069179	p < 1e-07	INPP4B inositol polyphosphate-4-phosphatase, type II, 105kD
NM_007210	p < 1e-07	GALNT6 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)
AI826254	p < 1e-07	HPN hepsin (transmembrane protease, serine 1)
AL080222	p < 1e-07	FLJ13110 hypothetical protein FLJ13110
AI082272	p < 1e-07	KIAA1467 KIAA1467 protein

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AF257081	p < 1e-07	KCNK15 potassium channel, subfamily K, member 15 (TASK-5)
AI439798	p < 1e-07	FGD3 FGD1 family, member 3
AI471793	p < 1e-07	Homo sapiens cDNA FLJ13598 fis, clone PLACE1009921
AI741657	p < 1e-07	ITPR1 inositol 1,4,5-triphosphate receptor, type 1
AK023655	p < 1e-07	FLJ13593 hypothetical protein FLJ13593
NM_006763	p < 1e-07	BTG2 BTG family, member 2
AK001783	p < 1e-07	FLJ10921 hypothetical protein FLJ10921
BC008814	p < 1e-07	SLC7A4 solute carrier family 7 (cationic amino acid transporter, y+ system), member 4
BC006526	p < 1e-07	SCNN1A sodium channel, nonvoltage-gated 1 alpha
AJ224171	p < 1e-07	LPHA lipophilin A (utero globin family member)
AI955511	0.0000003	ESTs
AA255953	p < 1e-07	ACADSB acyl-Coenzyme A dehydrogenase, short/branched chain
AJ249248	p < 1e-07	GPCR150 putative G protein-coupled receptor
AI276310	p < 1e-07	EST, Moderately similar to G02666 cysteine-rich protein 1 [H.sapiens]
R60224	0.0000001	ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]
AF224266	p < 1e-07	IL20 interleukin 20
AJ420562	p < 1e-07	PKIB protein kinase (cAMP-dependent, catalytic) inhibitor beta
AF052504	p < 1e-07	RNB6 RNB6
AI420473	p < 1e-07	EST
NM_014599	p < 1e-07	EHD4 EH-domain containing 4
AL080151	p < 1e-07	Homo sapiens mRNA, cDNA DKFZp434D024 (from clone DKFZp434D024)
BC012727	p < 1e-07	FLJ22593 hypothetical protein FLJ22593
AA574174	p < 1e-07	CYP2A7 cytochrome P450, subfamily 1A (phenobarbital-inducible), polypeptide 7
AI193043	p < 1e-07	ESTs, Weakly similar to T17226 hypothetical protein DKFZp566G223.1 [H.sapiens]
AF048700	p < 1e-07	SPINK4 serine protease inhibitor, Kazal type 4
AA860090	p < 1e-07	ESTs
AA904027	p < 1e-07	Homo sapiens cDNA FLJ30147 fis, clone BRACE2000266
NM_012244	p < 1e-07	SLC7A8 solute carrier family 7 (cationic amino acid transporter, y+ system), member 8
AI151349	p < 1e-07	ENPP1 ectonucleotide pyrophosphatase/phosphodiesterase 1
BC005395	p < 1e-07	HPX hemopexin
AI247880	p < 1e-07	F7 coagulation factor VII (serum prothrombin conversion accelerator)
AW207804	p < 1e-07	ESTs, Weakly similar to A36036 cytochrome P450 2F1 [H.sapiens]
AK025256	p < 1e-07	FLJ21603 hypothetical protein FLJ21603
BF434467	p < 1e-07	ESTs

AI799887	p < 1e-07	EST
AA804407	p < 1e-07	FLJ10980 hypothetical protein FLJ10980
AW138427	p < 1e-07	ESTs
BC010626	p < 1e-07	Homo sapiens, clone M3C:17687 IMAGE:3865868, mRNA, complete cds
BC009722	p < 1e-07	Homo sapiens, clone M3C:9575 IMAGE:3879368, mRNA, complete cds
BF129497	p < 1e-07	EST
BC014851	p < 1e-07	LFNG lunatic fringe homolog (Drosophila)
BF510534	p < 1e-07	UMOD uromodulin (uromucoid, Tamm-Horsfall glycoprotein)
AA627358	p < 1e-07	ESTs
AA846278	p < 1e-07	ESTs
AA933076	p < 1e-07	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
BC004143	p < 1e-07	[H.sapiens]
BC014607	p < 1e-07	BF B-factor, properdin
AA810085	p < 1e-07	ASP AKAP-associated sperm protein
AF070604	p < 1e-07	CXorf10 chromosome X open reading frame 10
BC001278	p < 1e-07	CACNA1H calcium channel, voltage-dependent, alpha 1H subunit
AF038191	p < 1e-07	SPUVE protease, serine, 23
BC013430	p < 1e-07	BAAP3 BAI1-associated protein 3
BC008962	p < 1e-07	UGDH UDP-glucose dehydrogenase
U45975	p < 1e-07	PLAB prostate differentiation factor
BF476394	p < 1e-07	PIB5PA phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A
BC006428	p < 1e-07	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
NM_004419	p < 1e-07	HSPC195 hypothetical protein
AL512743	0.0000054	DUSP5 dual specificity phosphatase 5
BC014213	p < 1e-07	SYT13 synaptotagmin XIII
NM_000352	p < 1e-07	RAB30 RAB30, member RAS oncogene family
X83301	p < 1e-07	ABCC8 ATP-binding cassette, sub-family C (CFTR/MRP), member 8
AL049265	p < 1e-07	SMA5 SMA5
AF237905	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp564F053 (from clone DKFZp564F053)
BC002738	p < 1e-07	MS4A8B membrane-spanning 4-domains, subfamily A, member 8B
BF476123	p < 1e-07	CRIP1 cysteine-rich protein 1 (intestinal)
AK026912	0.0000001	ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens]
AI254131	p < 1e-07	FLJ23259 hypothetical protein FLJ23259
		ESTs

AK027159	p < 1e-07	FLJ23506 hypothetical protein FLJ23506
BC004488	p < 1e-07	GRP gastrin-releasing peptide
AK021798	p < 1e-07	FLJ11736 hypothetical protein FLJ11736
AF007170	p < 1e-07	KIAA0452 DEME-6 protein
BC010607	p < 1e-07	Homo sapiens, clone MGC:18216 IMAGE:4156235, mRNA, complete cds
AK027311	p < 1e-07	KIAA1276 KIAA1276 protein
NM_057158	p < 1e-07	DUSP4 dual specificity phosphatase 4
AI198522	p < 1e-07	SLC11A3 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3
BC003513	0.0000003	SCYB14 small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK)
AI352080	p < 1e-07	FLJ14299 hypothetical protein FLJ14299
NM_002381	p < 1e-07	MATN3 matrin 3
L07738	p < 1e-07	CACNG1 calcium channel, voltage-dependent, gamma subunit 1
AI636974	p < 1e-07	LOC51097 CGI-49 protein
AF191017	0.0000007	H11 protein kinase H11
AI620482	p < 1e-07	EST
AW3300891	p < 1e-07	FLJ20753 hypothetical protein FLJ20753
BC005273	p < 1e-07	Homo sapiens, clone MGC:12318 IMAGE:3685423, mRNA, complete cds
AF367473	p < 1e-07	NYD-SP21 testes development-related NYD-SP21
AL137761	p < 1e-07	Homo sapiens mRNA, cDNA DKFZp586L2424 (from clone DKFZp586L2424)
AI468574	p < 1e-07	ESTs
AW292427	p < 1e-07	Homo sapiens cDNA FLJ13596 fis, clone PLACE1009637
AJ420423	p < 1e-07	Homo sapiens mRNA full length insert cDNA clone EUROIIMAGE 1287006
AI432615	p < 1e-07	DXS1283E GS2 gene
AW207201	p < 1e-07	CHAD chondroadherin
BC012900	p < 1e-07	Homo sapiens, clone IMAGE:3881549, mRNA
AI559487	p < 1e-07	SALL2 sal-like 2 (Drosophila)
AW194426	p < 1e-07	ESTs
NM_003225	p < 1e-07	TFF1 trefoil factor 1 (breast cancer, estrogen-inducible sequence expressed in)
AW270334	p < 1e-07	ESTs
BC013591	p < 1e-07	NTN4 netrin 4
NM_004923	p < 1e-07	MTL5 metallothionein-like 5, testis-specific (tesmin)
AI685841	p < 1e-07	ESTs
AW613732	p < 1e-07	Homo sapiens cDNA FLJ31137 fis, clone IMR322001049
AL133644	p < 1e-07	Homo sapiens mRNA, cDNA DKFZp434P1514 (from clone DKFZp434P1514); partial cds

AY048757	p < 1e-07	ABCG1 ATP-binding cassette, sub-family G (WHITE), member 1
AW292522	p < 1e-07	ESTs, highly similar to A55713 inositol 1,4,5-triphosphate receptor type 1 [H.sapiens]
BC001809	p < 1e-07	MGC3771 hypothetical protein MGC3771
AB038463	p < 1e-07	CAPN9 calpain 9 (nCL-4)
NM_033380	p < 1e-07	COL4A5 collagen, type IV, alpha 5 (Alport syndrome)
BC004240	p < 1e-07	CITED1 Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1
AF435925	p < 1e-07	VLGR1 very large G protein-coupled receptor 1
A1378647	p < 1e-07	ESTs
AF035408	p < 1e-07	CILP cartilage intermediate layer protein, nucleotide pyrophosphohydrolase
U11058	p < 1e-07	KCNMA1 potassium large conductance calcium-activated channel, subfamily M, alpha member 1
A1814187	p < 1e-07	KIAA1061 KIAA1061 protein
A1399653	p < 1e-07	ESTs
AL050090	p < 1e-07	DKFZP586F1018 DKFZP586F1018 protein
AY043361	p < 1e-07	WWP1 WW domain-containing protein 1
AK027241	p < 1e-07	FLJ23588 hypothetical protein FLJ23588
AK024892	p < 1e-07	SH3BGR1 SH3 domain binding glutamic acid-rich protein like
A1928365	0.0000003	SLC1A1 solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1
BE675157	p < 1e-07	ESTs
A1669410	p < 1e-07	ESTs
AA826324	p < 1e-07	Homo sapiens cDNA FLJ32320 fis, clone PROST2003537
BC009203	p < 1e-07	LOC90355 hypothetical gene supported by AF038182; BC009203
A1828600	p < 1e-07	ESTs
AK026141	p < 1e-07	Homo sapiens cDNA: FLJ22488 fis, clone HRC10948, highly similar to HSU79298 Human clone 23803 mRNA
A1208471	0.0000001	HRLP5 H-rev107-like protein 5
AK000978	p < 1e-07	FLJ10116 hypothetical protein FLJ10116
AL136579	p < 1e-07	KIAA1415 KIAA1415 protein
		CYP21A2 cytochrome P450, subfamily XXIA (steroid 21-hydroxylase, congenital adrenal hyperplasia), polypeptide 2
A1479704	p < 1e-07	SEZ6L seizure related 6 homolog (mouse)-like
AW148827	p < 1e-07	BEX1 brain expressed, X-linked 1
AF220189	0.0000329	EST
AA557341	p < 1e-07	MGC11138 hypothetical protein MGC11138
BC004504	p < 1e-07	Homo sapiens cDNA FLJ30298 fis, clone BRACE2003172
A1922204	0.0000002	NELL2 NEL-like 2 (chicken)
A1969835	0.0000003	

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NM_000841	0.0000012	GRM4 glutamate receptor, metabotropic 4
AW205768	0.0000269	THRSP thyroid hormone responsive (SPOT14 homolog, rat)
AF100759	p < 1e-07	NET-6 tetraspan NET-6 protein
AF121129	p < 1e-07	NR2E3 nuclear receptor subfamily 2, group E, member 3
		Homo sapiens cDNA FLJ31235 fis, clone KIDNE2004681, moderately similar to Mus musculus peroxisomal long chain acyl-CoA thioesterase 1b (Ple1b) gene
AI126271	p < 1e-07	Homo sapiens cDNA FLJ33115 fis, clone TRACH2001314
AI457338	p < 1e-07	Homo sapiens cDNA FLJ11375 fis, clone HEMBA1000411, weakly similar to ANKYRIN
BM126815	p < 1e-07	FLJ10244 hypothetical protein FLJ10244
BF002534	p < 1e-07	SLC6A4 solute carrier family 6 (neurotransmitter transporter, serotonin), member 4
AA700070	0.0000066	Homo sapiens, Similar to synaptotagmin-like 4, clone MGC:17313 IMAGE:3908307, mRNA, complete cds
BC014913	p < 1e-07	GALNAC4S-6ST B cell RAG associated protein
AF026477	p < 1e-07	ESTs
R16838	p < 1e-07	C8orf4 chromosome 8 open reading frame 4
AF116660	0.0000006	ENPP5 ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function)
AI568799	p < 1e-07	ESTs
AA633845	p < 1e-07	ESTs
AW265341	p < 1e-07	SCAP1 src family associated phosphoprotein 1
AA738043	p < 1e-07	Homo sapiens cDNA: FLJ21346 fis, clone COL02705
AK024999	p < 1e-07	CACNA1D calcium channel, voltage-dependent, L type, alpha 1D subunit
M76558	p < 1e-07	PACE4 paired basic amino acid cleaving system 4
AW016396	p < 1e-07	ESTs
H04392	p < 1e-07	RTN1 reticulon 1
BC000314	0.0000001	GPR54 G protein-coupled receptor 54
AI823800	0.0000002	FLJ10058 hypothetical protein FLJ10058
AW135596	p < 1e-07	KIAA0239 KIAA0239 protein
AI364725	p < 1e-07	Homo sapiens cDNA FLJ32802 fis, clone TESTI2002580
AI200759	p < 1e-07	IRS1 insulin receptor substrate 1
NM_005544	p < 1e-07	EIF4B eukaryotic translation initiation factor 4B
AA580157	p < 1e-07	EST
AI926614	p < 1e-07	VAV3 vav 3 oncogene
NM_006113	p < 1e-07	RAB5EP rabaptin-5
AW007851	p < 1e-07	Homo sapiens, clone MGC:16638 IMAGE:4121964, mRNA, complete cds
BC009373	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp434N2412 (from clone DKFZp434N2412)
AL157499	p < 1e-07	

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BC015520	p < 1e-07	RNASE4 ribonuclease, RNase A family, 4
AB050468	p < 1e-07	LIG1 ortholog of mouse integral membrane glycoprotein LIG-1
AI446183	p < 1e-07	ESTs, Highly similar to C7A5_HUMAN ADENYLATE CYCLASE, TYPE V [H.sapiens]
AI806109	0.0000003	KIAA1580 KIAA1580 protein
AI479419	p < 1e-07	KIAA1511 KIAA1511 protein
AL136858	p < 1e-07	DKFZp434N2435 hypothetical protein DKFZp434N2435
BI491333	p < 1e-07	Homo sapiens cDNA FLJ13289 fts, clone OVARC1001170
AF035282	p < 1e-07	C1orf21 chromosome 1 open reading frame 21
R36615	p < 1e-07	ESTs
AI673455	p < 1e-07	ESTs
BC000809	p < 1e-07	TCEAL1 transcription elongation factor A (SII)-like 1
AW450693	p < 1e-07	Homo sapiens mRNA, exon 1, 2, 3, 4, clone:RES4-24A
		ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
AV646597	p < 1e-07	KIAA0040 KIAA0040 gene product
AA749341	p < 1e-07	QDPR quinoid dihydropteridine reductase
BC000576	p < 1e-07	SERPINA3 serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3
BC003559	p < 1e-07	HOXB5 homeo box B5
BC008940	0.0000051	SLC22A5 solute carrier family 22 (organic cation transporter), member 5
AF057164	p < 1e-07	SLC26A3 solute carrier family 26, member 3
L02785	0.0000373	TEKT2 tektin 2 (testicular)
AF054910	p < 1e-07	PTPRN2 protein tyrosine phosphatase, receptor type, N polypeptide 2
NM_002847	p < 1e-07	ANKHZN ANKHZN protein
AA775255	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp434B102 (from clone DKFZp434B102)
AL080192	p < 1e-07	MGC16309 hypothetical gene MGC16309
AK027206	p < 1e-07	C20orf103 chromosome 20 open reading frame 103
BE671061	p < 1e-07	VIPR2 vasoactive intestinal peptide receptor 2
X95097	0.0000007	GLI3 GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome)
M57609	p < 1e-07	SLC2A10 solute carrier family 2 (facilitated glucose transporter), member 10
AF248053	p < 1e-07	Homo sapiens cDNA FLJ12379 fts, clone MAMMA1002554
AK022441	p < 1e-07	NMES1 normal mucosa of esophagus specific 1
AB026707	p < 1e-07	RPH3AL rabphilin 3A-like (without C2 domains)
BC005153	p < 1e-07	ESTs
AW449824	p < 1e-07	SEC14L2 SEC14-like 2 (S. cerevisiae)
AW080831	p < 1e-07	

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AI674226	p < 1e-07	Homo sapiens, Similar to RIKEN cdNA 1700008D07 gene, clone MGC:9830 IMAGE:3863323, mRNA, complete cds
AI382972	p < 1e-07	TPBG trophoblast glycoprotein
AK025198	0.0000003	Homo sapiens cDNA: FLJ21545 fs, clone COL06195
BC000662	p < 1e-07	MGC2601 hypothetical protein MGC2601
AL133622	p < 1e-07	KIAA0876 KIAA0876 protein
R42185	p < 1e-07	Homo sapiens cDNA FLJ32064 fs, clone OCBBF1000080
U62325	p < 1e-07	APBB2 amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)
BC008317	p < 1e-07	LIV-1 LIV-1 protein, estrogen regulated
AI825621	0.0000001	KIAA1130 KIAA1130 protein
M93119	0.0006433	INSM1 insulinoma-associated 1
BC016018	p < 1e-07	Homo sapiens, clone M5C:27478 IMAGE:4714682, mRNA, complete cds
D89675	p < 1e-07	BMFPR1B bone morphogenetic protein receptor, type 1B
AI093769	p < 1e-07	ESTs
NM_006006	0.0000002	ZNF145 zinc finger protein 145 (Kruppel-like, expressed in promyelocytic leukemia)
AW294857	p < 1e-07	LOC51161 g20 protein
AK000269	p < 1e-07	FLJ20262 hypothetical protein FLJ20262
AI674190	p < 1e-07	FLJ13941 hypothetical protein FLJ13941
AW207696	0.0000453	MGB2 magmaglobin 2
R41429	p < 1e-07	ATP7E ATPase, Cu++ transporting, beta polypeptide (Wilson disease)
AF131784	p < 1e-07	Homo sapiens clone 25194 mRNA sequence
BC010963	0.0000002	TNNT1 troponin T1, skeletal, slow
BC009799	0.0000392	AREG amphiregulin (schwannoma-derived growth factor)
AJ278018	p < 1e-07	CS2 calstylenin-2
BI494440	p < 1e-07	KIAA0222 KIAA0222 gene product
AF140240	p < 1e-07	TBX3 T-box 3 (ulnar mammary syndrome)
D50840	p < 1e-07	UGCG UDP-glucose ceramide glucosyltransferase
AW157331	p < 1e-07	KIAA1246 KIAA1246 protein
AW074266	p < 1e-07	ESTs
BF110928	p < 1e-07	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
AI961444	p < 1e-07	P37NB 37 kDa leucine-rich repeat (LRR) protein
AK027251	p < 1e-07	FLJ23598 hypothetical protein FLJ23598
AF131832	p < 1e-07	DKFZp761F2014 hypothetical protein DKFZp761F2014
AI866858	0.0000002	MUC1 mucin 1, transmembrane

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AI688494	0.0000005	FLJ13189 hypothetical protein FLJ13189
AW150267	0.0000037	C21orf9 chromosome 21 open reading frame 9
		Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs, the gene for a novel BZRP (peripheral benzodiazepine receptor (MBR,PBR, PBKS, IBP, Isoquinoline-binding protein)) LIKE protein, the gene for a novel protein similar to part of APOBEC1 (Phorbol 1, Apolipoprotein B mRNA editing protein), and the NFYA gene for nuclear transcription factor Y, alpha (CCAAT-Binding transcription factor subunit B, CBF-B, CAAT-Box DNA binding protein subunit A). Contains ESTs, STSs, GSSs, two putative CpG islands and a ca repeat polymorphism
AI038082	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp564O1763 (from clone DKFZp564O1763)
AL110139	p < 1e-07	CPLX1 complexin 1
BC002471	p < 1e-07	PDEF prostate epithelium-specific Ets transcription factor
AB031549	p < 1e-07	HGD homogentisate 1,2-dioxygenase (homogentisate oxidase)
U63008	0.0000033	SLC19A2 solute carrier family 19 (thiamine transporter), member 2
AF153330	p < 1e-07	FLJ23462 duodenal cytochrome b
AL136693	p < 1e-07	HEP27 short-chain alcohol dehydrogenase family member
BC007339	0.0000001	MRPS30 mitochondrial ribosomal protein S30
AF146192	p < 1e-07	NBEA neurobeachin
AL137748	p < 1e-07	ESTs
AI989600	p < 1e-07	ESTs
AW469017	p < 1e-07	HSPA2 heat shock 70kD protein 2
U56725	0.0000001	KIAA0303 KIAA0303 protein
AK057601	p < 1e-07	ESTs
AI147370	p < 1e-07	ADCY1 adenylate cyclase 1 (brain)
AA497018	p < 1e-07	PLAC1 placenta-specific 1
BF510257	0.0000001	KCND2 potassium voltage-gated channel, Shal-related subfamily, member 2
AB028967	0.0000032	TFAP2B transcription factor AP-2 beta (activating enhancer binding protein 2 beta)
NM_003221	0.0004633	ESTs
AI349306	0.0000004	ASPN asporin (LRR class 1)
AY029191	0.0000011	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
BG272534	p < 1e-07	RFX2 regulatory factor X, 2 (influences HLA class II expression)
AI288717	p < 1e-07	KIAA0938 KIAA0938 protein
AI080649	p < 1e-07	DKFZP586J0619 DKFZP586J0619 protein
AA177001	p < 1e-07	ESTs
AW340797	0.0000006	ESTs

N95437	0.000001	ESTs
BC016153	0.0000058	Homo sapiens, Similar to hypothetical protein FLJ10134, clone MGC:13208 IMAGE:3841102, mRNA, complete cds
AL136592	p < 1e-07	DKFZP7611172 hypothetical protein DKFZp7611172
AI217517	p < 1e-07	KIAA0557 KIAA0557 protein
AI128331	p < 1e-07	ENDOFIN endosome-associated FYVE-domain protein
BF446355	p < 1e-07	ESTs
AK000634	p < 1e-07	FLJ20627 hypothetical protein FLJ20627
AI655104	p < 1e-07	ESTs
AL136901	p < 1e-07	FLJ22944 hypothetical protein FLJ22944
NM_000909	0.0000001	NPY1R neuropeptide Y receptor Y1
AI379600	p < 1e-07	FLJ11715 hypothetical protein FLJ11715
AF098277	p < 1e-07	SLC23A2 solute carrier family 23 (nucleobase transporters), member 2
AI631667	p < 1e-07	Homo sapiens cDNA FLJ31763 fis, clone NT2R12007827
AL157484	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp762M127 (from clone DKFZp762M127)
AY040546	0.0001123	Homo sapiens RPE-spondin (RPESP) mRNA, partial cds
AI373939	0.00001	GJA1 gap junction protein, alpha 1, 43kD (connexin 43)
NM_001322	p < 1e-07	GST2 cystatin SA
U96136	0.0000023	CTNND2 catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)
AB038518	p < 1e-07	COLEC12 collectin sub-family member 12
AI332972	p < 1e-07	Homo sapiens, clone MGC:9889 IMAGE:3868330, mRNA, complete cds
AL161952	p < 1e-07	GLUL glutamate-ammonia ligase (glutamine synthase)
BE464993	p < 1e-07	Homo sapiens PAC, clone RP4-751H13, from 7q35-qter
AI394310	p < 1e-07	GALNT7 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)
AW149773	0.0000001	p25 brain-specific protein p25 alpha
Y17978	p < 1e-07	FUT8 fucosyltransferase 8 (alpha (1,6) fucosyltransferase)
AF183421	p < 1e-07	RAB31 RAB31, member RAS oncogene family
BE676675	p < 1e-07	RIPK3 receptor-interacting serine-threonine kinase 3
AL096739	p < 1e-07	DKFZp586H0623 putative UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase T9
R37016	0.0000002	KIAA0534 KIAA0534 protein
AB018286	0.0000069	NRXN3 neuexin 3
AK026842	p < 1e-07	FLJ23189 hypothetical protein FLJ23189
NM_003489	p < 1e-07	NR1P1 nuclear receptor interacting protein 1
D86322	0.0000004	CLGN calmegin

AI951144	p < 1e-07	ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]
AA706017	p < 1e-07	ESTs
AA631782	0.0000004	EST
AL117550	p < 1e-07	LOC51643 CGI-119 protein
		ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
AI000682	p < 1e-07	[H.sapiens]
AJ420490	0.0000818	IL20RA interleukin 20 receptor, alpha
AY007114	p < 1e-07	Homo sapiens clone TCCCTA00151 mRNA sequence
AF035299	p < 1e-07	DOK1 docking protein 1, 62kD (downstream of tyrosine kinase 1)
AI039854	p < 1e-07	SYNCOILIN intermediate filament protein syncoilin
AW139266	p < 1e-07	FLJ12057 hypothetical protein FLJ12057
NM_003961	p < 1e-07	RHBDL rhomboid, veinlet-like 1 (Drosophila)
AI277269	p < 1e-07	KIAA0944 KIAA0944 protein
AF153605	p < 1e-07	AIg-1 androgen induced protein
M60445	0.0000066	HDC histidine decarboxylase
BC002668	p < 1e-07	PECI peroxisomal D3,D2-enoyl-CoA isomerase
AW296675	p < 1e-07	NUCB2 nucleobindin 2
BE464662	p < 1e-07	ESTs
AW205080	p < 1e-07	NEURL neuralized-like (Drosophila)
Y10183	p < 1e-07	ALCAM activated leucocyte cell adhesion molecule
AL137449	0.0000081	HOXB4 homeo box B4
AF004222	p < 1e-07	RTN2 reticulon 2
AK022482	p < 1e-07	Homo sapiens cDNA FLJ12420 fis, clone MAMMA1003049
NM_007069	p < 1e-07	HRASLS3 HRAS-like suppressor 3
NM_001231	p < 1e-07	CASQ1 calsequestrin 1 (fast-twitch, skeletal muscle)
AL136760	p < 1e-07	DKFZP434H0115 hypothetical protein DKFZp434H0115
AI244129	0.0000001	RAMP3 receptor (calcitonin) activity modifying protein 3
BC000548	0.0000002	RAMP1 receptor (calcitonin) activity modifying protein 1
BC005257	0.0000724	MSMB microseminoprotein, beta-
AF116574	p < 1e-07	ASTN2 astrotactin 2
AA782483	p < 1e-07	REPS2 RALBP1 associated Eps domain containing 2
AI912086	p < 1e-07	Homo sapiens cDNA FLJ30744 fis, clone FEBRA2000378
U78168	p < 1e-07	EPAC Rap1 guanine-nucleotide-exchange factor directly activated by cAMP
AA016043	p < 1e-07	SAG S-antigen; retina and pineal gland (arrestin)

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NM_003155	0.0000041	STC1 stanniocalcin 1
BE672557	p < 1e-07	ESTs
AK026275	p < 1e-07	FLJ22622 hypothetical protein FLJ22622
AA993573	p < 1e-07	TGFB3 transforming growth factor, beta 3
BC018043	0.0000003	SERPIN1 serine (or cysteine) proteinase inhibitor, clade I (neuroserpin), member 1
BC006168	p < 1e-07	KIAA0089 KIAA0089 protein
AW206445	p < 1e-07	ESTs, Weakly similar to UOG1_HUMAN UOG-1 PROTEIN [H.sapiens]
AA513133	p < 1e-07	ESTs, Weakly similar to 1209280A tropomyosin [H.sapiens]
AL080094	0.0000673	Homo sapiens mRNA, cDNA DKFZp564O1262 (from clone DKFZp564O1262)
BC009211	p < 1e-07	ELP2 elongator protein 2
BC004161	p < 1e-07	NET-7 transmembrane 4 superfamily member (tetraspan NET-7)
NM_001094	0.0000052	ACCN1 amiloride-sensitive cation channel 1, neuronal (degenerin)
AL136539	p < 1e-07	DKFZF761E2110 hypothetical protein DKFZF761E2110
AA846880	p < 1e-07	MEIS3 Meis1, myeloid ecotropic viral integration site 1 homolog 3 (mouse)
AF144094	p < 1e-07	MYO15A myosin XVa
AF159570	0.0000001	RGS5 regulator of G-protein signaling 5
AW015327	p < 1e-07	IGF1R insulin-like growth factor 1 receptor
AK021540	p < 1e-07	Homo sapiens cDNA FLJ11478 fis, clone HEMBA1001781
BC007618	0.0000001	MGC15730 hypothetical protein MGC15730
NM_001899	p < 1e-07	CST4 cystatin S
R74353	p < 1e-07	HNMT histamine N-methyltransferase
AI262988	p < 1e-07	KIAA1548 KIAA1548 protein
AA505938	p < 1e-07	EST
AI866828	0.0000073	COL10A1 collagen, type X, alpha 1 (Schmid metaphyseal chondrodysplasia)
AI076506	0.0000001	RORC RAR-related orphan receptor C
AJ245503	0.0000001	PXR2b PXR2b protein
AF217970	p < 1e-07	Homo sapiens clone PP1195 unknown mRNA
AI963850	p < 1e-07	KIAA1324 KIAA1324 protein
U80811	p < 1e-07	EDG2 endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2
AA745593	p < 1e-07	BATF basic leucine zipper transcription factor, ATF-like
AW328488	0.0000002	PTK6 PTK6 protein tyrosine kinase 6
AA258057	p < 1e-07	ESTs
AW104057	p < 1e-07	ESTs
AK027148	p < 1e-07	FLJ23495 hypothetical protein FLJ23495

AW070918	p < 1e-07	ESTs, Weakly similar to T2D3_HUMAN TRANSCRIPTION INITIATION FACTOR TFIIID 135 KDA SUBUNIT [H.sapiens]
AI369214	p < 1e-07	ESTs
BC002591	0.0001249	MMP10 matrix metalloproteinase 10 (stromelysin 2)
AA431407	0.0000011	MACS1 medium-chain acyl-CoA synthetase
BC016955	p < 1e-07	Homo sapiens cDNA: FLJ22182 fis, clone HRC00953
AI033912	0.0000003	RLN2 relaxin 2 (H2)
AA600175	0.0000428	ESTs
AI436323	0.0000487	ROBO2 roundabout, axon guidance receptor, homolog 2 (Drosophila)
AL136939	p < 1e-07	HELO1 homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2
AI471839	p < 1e-07	THBD thrombomodulin
S61953	p < 1e-07	ERBB3 v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)
AA595802	p < 1e-07	ESTs, Weakly similar to T17279 hypothetical protein DKFZp434F1935.1 [H.sapiens]
AA865325	p < 1e-07	RAMP2 receptor (calcitonin) activity modifying protein 2
AI866867	0.0000002	SEMA3C sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C
AI768204	0.000014	CDSN corneodesmosin
AI200391	0.0000004	ESTs, Weakly similar to S26689 hypothetical protein hc1 - mouse [M.musculus]
AI670779	p < 1e-07	ESTs, Weakly similar to ALUC_HUMAN [iii] ALU CLASS C WARNING ENTRY [ii] [H.sapiens]
BC010924	0.0000001	PRO1073 PRO1073 protein
NM_006103	0.0000086	WFDC2 WAP four-disulfide core domain 2
AI955538	p < 1e-07	Homo sapiens cDNA FLJ33142 fis, clone UTERU1000192
BC010522	p < 1e-07	Homo sapiens, clone MGC:18084 IMAGE:4150952, mRNA, complete cds
		Homo sapiens cDNA FLJ31149 fis, clone IMR322001491, moderately similar to Rattus norvegicus tricarboxylate carrier-like protein mRNA
N89991	p < 1e-07	PCANAP1 prostate cancer associated protein 1
AK026813	p < 1e-07	HSD17B4 hydroxysteroid (17-beta) dehydrogenase 4
BC003098	p < 1e-07	FLJ23403 hypothetical protein FLJ23403
AK027056	0.0000001	SERHL kraken-like
AA582929	0.0000095	Homo sapiens cDNA FLJ13603 fis, clone PLACE1010270
AV656862	p < 1e-07	ESTs
AI686160	p < 1e-07	ESTs
R42732	p < 1e-07	FLJ21347 hypothetical protein FLJ21347
AK025000	p < 1e-07	SDCAG28 serologically defined colon cancer antigen 28
AW247958	p < 1e-07	EST, Moderately similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING
AI804711	p < 1e-07	

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BC010553	0.0000179	ENTRY [H.sapiens] TIMP4 tissue inhibitor of metalloproteinase 4 Homo sapiens cDNA: FLJ23371 fis, clone HEP16068, highly similar to HSTFISH Homo sapiens mRNA for transcription elongation factor TFIIIS
AK027024	p < 1e-07	
AL133591	0.0000241	Homo sapiens mRNA; cDNA DKFZp434N079 (from clone DKFZp434N079)
AW513195	p < 1e-07	Homo sapiens cDNA FLJ13524 fis, clone PLACE1006002
AI866286	p < 1e-07	ESTs, Weakly similar to CA13 MOUSE COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [M.musculus]
AL583912	p < 1e-07	KIF13B kinesin family member 13B
NM_018653	0.0000004	GPRC5C G protein-coupled receptor, family C, group 5, member C
AI218954	p < 1e-07	KIAA0717 KIAA0717 protein
AJ420566	p < 1e-07	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1572223
BF447150	0.0000017	ESTs
AK025296	p < 1e-07	FLJ20273 hypothetical protein
AK025732	p < 1e-07	ASAH N-acylsphingosine amidohydrolase (acid ceramidase)
AK001648	p < 1e-07	FLJ10786 hypothetical protein FLJ10786
BC015182	p < 1e-07	CYB5 cytochrome b-5
R56053	0.0000002	ME3 malic enzyme 3, NADP(+)-dependent, mitochondrial
AW450080	0.0000018	Human clone 137308 mRNA, partial cds
NM_033014	0.0000032	OGN osteoglycin (osteoinductive factor, mimecan)
AK026817	p < 1e-07	FLJ23577 hypothetical protein FLJ23577
R61469	0.0000454	Human (clone CTG-A4) mRNA sequence
BC002619	0.000176	LOC51617 HMP19 protein
AI150439	p < 1e-07	KIAA1407 KIAA1407 protein
BC017338	p < 1e-07	FUCA1 fucosidase, alpha-L-1, tissue
AF117708	p < 1e-07	KCNK6 potassium channel, subfamily K, member 6 (TWIK-2)
AW139414	p < 1e-07	PRLR prolactin receptor
AI559968	p < 1e-07	RGL3 RalGEF-like protein 3, mouse homolog
AW195539	p < 1e-07	DDO D-aspartate oxidase
AK024964	p < 1e-07	NFIA nuclear factor I/A
BC004925	0.0000004	Homo sapiens, Similar to G protein-coupled receptor, family C, group 5, member C, clone MGC:10304
AJ420521	0.0000005	IMAGE:3622005, mRNA, complete cds
AF271783	p < 1e-07	SMOC2 secreted modular calcium-binding protein 2
AA883246	0.0000032	FLJ21174 hypothetical protein FLJ21174 Homo sapiens cDNA FLJ30428 fis, clone BRACE2008941

AW050970	0.0000062	DF D component of complement (adipsin)
BC016615	p < 1e-07	Homo sapiens, Similar to FAB37, member of RAS oncogene family, clone MGC:21391 IMAGE:4520191, mRNA, complete cds
A1972866	p < 1e-07	ESTs
AA554481	0.0000003	ESTs
NM_014279	0.0000094	OLF1 olfactomedin 1
A1628869	p < 1e-07	FLJ12953 hypothetical protein FLJ12953 similar to Mus musculus D3Mm3e
AL133636	p < 1e-07	CIRBP cold inducible RNA binding protein
AW148329	p < 1e-07	ESTs
AL043469	0.0000007	F13A1 coagulation factor XIII, A1 polypeptide
BC005989	0.0001701	PNLIPRP2 pancreatic lipase-related protein 2
AL133033	p < 1e-07	KIAA1025 KIAA1025 protein
A1536750	0.0000003	ROR2 receptor tyrosine kinase-like orphan receptor 2
BC001638	0.000447	ASCL1 achaete-scute complex-like 1 (Drosophila)
BC008185	p < 1e-07	FABGL FabG (beta-ketoacyl-[acyl-carrier-protein] reductase, E coli) like (E. coli)
AA399226	p < 1e-07	TJP3 tight junction protein 3 (zona occludens 3)
NM_003979	p < 1e-07	RAI3 retinoic acid induced 3
A1367233	p < 1e-07	EST
BC018636	p < 1e-07	PLAT plasminogen activator, tissue
A1565489	p < 1e-07	PDE4A phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)
AW136191	p < 1e-07	ESTs
A1421708	p < 1e-07	Homo sapiens cDNA FLJ13137 fis, clone NT2RP3003150
AW057705	0.0000003	FLT3 fms-related tyrosine kinase 3
AA843666	0.0000031	ESTs
BC000232	p < 1e-07	D5S346 DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis
AB023416	p < 1e-07	ASC apoptosis-associated speck-like protein containing a CARD
AL049987	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp564F112 (from clone DKFZp564F112)
AF261655	p < 1e-07	HMIC 1,2-alpha-mannosidase IC
AK025683	0.0000001	Homo sapiens cDNA: FLJ22030 fis, clone HEP08669
AA401311	0.0000002	KIAA1377 KIAA1377 protein
BF446757	p < 1e-07	ESTs
AW076080	p < 1e-07	Homo sapiens, clone IMAGE:3463399, mRNA, partial cds
BC009778	0.0000007	LOC51207 protein phosphatase
X13897	0.0000008	CYP2A6 cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6

AW450142	0.0000002	SLC22A4 solute carrier family 22 (organic cation transporter), member 4
AA086248	0.0000009	ESTs
AW150018	0.0000001	FMOD fibromodulin
AA831831	p < 1e-07	MORF histone acetyltransferase
AL050143	p < 1e-07	DKFZP586B2420 DKFZP586B2420 protein
AL110252	0.0000155	Homo sapiens mRNA; cDNA DKFZp556A1046 (from clone DKFZp556A1046)
M92432	0.0000243	GUCY2D guanylate cyclase 2D, membrane (retina-specific)
AI185187	p < 1e-07	LOC51133 NY-REN-45 antigen
AF094758	p < 1e-07	NESG1 nasopharyngeal epithelium specific protein 1
BC012541	0.0000005	ALEX2 armadillo repeat protein ALEX2
AW140108	0.0000121	HOXD8 homeo box D8
AF212239	0.0000254	RBP5 retinol binding protein 5, cellular
AK000207	p < 1e-07	FLJ20200 hypothetical protein FLJ20200
BC002842	0.0000004	H2BFB3 H2B histone family, member B
AI263595	0.0000118	ESTs
AL136911	p < 1e-07	EPLIN epithelial protein lost in neoplasm beta
NM_004694	p < 1e-07	SLC16A6 solute carrier family 16 (monocarboxylic acid transporters), member 6
BC007323	0.0000001	NDUFEC2 NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b)
AI474354	0.0000155	TSLRP testis specific leucine rich repeat protein
NM_004430	0.0000026	EGR3 early growth response 3
BM128958	p < 1e-07	KIAA1643 KIAA1643 protein
AL360141	p < 1e-07	PEX11A peroxisomal biogenesis factor 11A
BC000465	p < 1e-07	GADD45G growth arrest and DNA-damage-inducible, gamma
AI629046	p < 1e-07	EMX1 empty spiracles homolog 1 (Drosophila)
AF267859	0.0000002	FLJ13153 hypothetical protein FLJ13153
AA654227	p < 1e-07	BCAS4 breast carcinoma amplified sequence 4
U38276	p < 1e-07	SEMA3F sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F
NM_053056	p < 1e-07	CCND1 cyclin D1 (PRAD1: parathyroid adenomatosis 1)
AL117393	p < 1e-07	KIF5C kinesin family member 5C
AI921122	0.0000001	ESTs, Highly similar to dJ25J6.2 [H.sapiens]
BC009381	0.0000055	STMN3 stathmin-like 3
AW207140	0.0000101	ARNT2 aryl-hydrocarbon receptor nuclear translocator 2
AW083384	p < 1e-07	ESTs, Moderately similar to T46395 hypothetical protein DKFZp4341120.1 [H.sapiens]
AJ420536	p < 1e-07	Homo sapiens mRNA full length insert cDNA clone EUROIIMAGE 994183

022041001010PC

AI561078	p < 1e-07	TSPAN-1 tetraspan 1
AK000209	p < 1e-07	FLJ20202 hypothetical protein FLJ20202
AI674472	p < 1e-07	EST
R40176	0.0000412	Homo sapiens cDNA FLJ32051 fis, clone NTONG2001428
NM_003248	0.0000968	THBS4 thrombospondin 4
AK023243	p < 1e-07	FLJ13181 hypothetical protein FLJ13181
AB000509	p < 1e-07	TRAF5 TNF receptor-associated factor 5
AA400069	0.0000004	FLJ13031 hypothetical protein FLJ13031
AA846684	p < 1e-07	ESTs
AI744756	p < 1e-07	ESTs
AK001889	0.0000002	Homo sapiens cDNA FLJ11027 fis, clone PLACE1004114
AA557345	0.0000009	EST, Weakly similar to 2109260A B cell growth factor [H.sapiens]
NM_012168	0.0000109	FBXO2 F-box only protein 2
BF475464	p < 1e-07	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
AL050116	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp586A131 (from clone DKFZp586A131)
NM_001089	p < 1e-07	ABCA3 ATP-binding cassette, sub-family A (ABC1), member 3
BC017586	0.0000002	Homo sapiens, Similar to RIKEN cDNA 1700028N11 gene, clone MGC:26610 IMAGE:4837506, mRNA, complete cds
AW006452	0.0000006	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]
AI097387	p < 1e-07	PRO1489 hypothetical protein PRO1489
AA601573	p < 1e-07	ESTs
AW080826	p < 1e-07	KIAA0984 KIAA0984 protein
AI809547	0.0000005	ESTs
AJ420459	p < 1e-07	LOC51184 protein x 0004
BE856073	p < 1e-07	STK39 serine threonine kinase 39 (STE20/SPS1 homolog, yeast)
AK000416	0.0000062	SLC16A5 solute carrier family 16 (monocarboxylic acid transporters), member 5
AW291846	p < 1e-07	C21orf15 chromosome 21 open reading frame 15
AI971681	0.0000003	PLCE phospholipase C, epsilon
AL157455	0.0000004	Homo sapiens mRNA; cDNA DKFZp7611912 (from clone DKFZp7611912)
AI823660	0.0000048	Homo sapiens cDNA: FLJ22133 fis, clone HEP20529
AF137027	0.0000933	TCL1B T-cell leukemia/lymphoma 1B
AF161423	p < 1e-07	PTD002 PTD002 protein
NM_006186	0.0000034	NR4A2 nuclear receptor subfamily 4, group A, member 2

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BC009522	0.0000046	SSTF2 somatostatin receptor 2
AI783781	0.0002071	EST
AL157492	p < 1e-07	DKFZP434P0111 hypothetical protein DKFZp434P0111
AK000691	p < 1e-07	FLJ22174 hypothetical protein FLJ22174
BC004312	0.0000013	IGFBP2 insulin-like growth factor binding protein 2 (36kD)
AA973836	0.0001602	ESTs
AL049223	p < 1e-07	SCAMP1 secretory carrier membrane protein 1
AI650407	p < 1e-07	ESTs
AA054983	p < 1e-07	EST
AA643697	0.000009	ESTs
BC000059	0.0000092	CELSR1 cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)
BC008703	p < 1e-07	MGC15737 hypothetical protein MGC15737
AK054785	p < 1e-07	Homo sapiens cDNA FLJ30223 fis, clone BRACE2001785
AK025209	p < 1e-07	Homo sapiens cDNA: FLJ21556 fis, clone COL06353
AY033290	p < 1e-07	LABH1 lung alpha/beta hydrolase 1
AW074143	0.0000002	ESTs
AL137419	0.0001168	C12orf3 chromosome 12 open reading frame 3
		ESTs, Weakly similar to YEX0_YEAST HYPOTHETICAL 64.8 KDA PROTEIN IN GDI1-COX15 INTERGENIC REGION [S.cerevisiae]
AI031941	p < 1e-07	ESTs, Weakly similar to Z195_HUMAN ZINC FINGER PROTEIN 195 [H.sapiens]
BF511644	p < 1e-07	RBSK ribokinase
BF436282	p < 1e-07	KAL1 Kallmann syndrome 1 sequence
AA854788	p < 1e-07	ESTs
H08145	0.0000011	MS4A2 membrane-spanning 4-domains, subfamily A, member 1
NM_000139	0.0000023	FGFR3 fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
NM_000142	0.000013	ESTs
AI204186	0.0001851	Homo sapiens, clone MGC:2492 IMAGE:3353520, mRNA, complete cds
AI341790	p < 1e-07	KIAA1372 KIAA1372 protein
AI499814	p < 1e-07	Homo sapiens, clone MGC:20208 IMAGE:3936339, mRNA, complete cds
BC014000	p < 1e-07	CBFA2T3 core-binding factor, runt domain, alpha subunit 2; translocated to, 3
AI221721	0.0000001	ESTs
AW139237	0.000015	ESTs
AA910336	0.0000163	ESTs
AK022443	0.0000003	Homo sapiens cDNA FLJ12381 fis, clone MAMMA1002566
AL133030	0.0000029	KIAA1666 KIAA1666 protein

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AK025532	p < 1e-07	FLJ21213 hypothetical protein FLJ21213
AL119854	0.0000017	KIAA1789 KIAA1789 protein
AA613425	0.0000152	COMP cartilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple)
AF245044	p < 1e-07	HT023 hypothetical protein HT023
AI951472	p < 1e-07	FLJ10724 melanoma antigen recognized by T cells 2
AK026216	p < 1e-07	Homo sapiens cDNA: FLJ22563 fis, clone HSI01928
BC017772	0.0000182	HT021 HT021
AI810347	p < 1e-07	ESTs. Weakly similar to ABP2_HUMAN ENDOTHELIAL ACTIN-BINDING PROTEIN [H.sapiens]
X86163	0.0000009	BDKRB2 bradykinin receptor B2
U67784	0.0000164	RDC1 G protein-coupled receptor
BC013083	p < 1e-07	CST3 cystatin C (amyloid angiopathy and cerebral hemorrhage)
AK025047	0.0000001	FLJ21394 hypothetical protein FLJ21394
AF288571	0.0000002	LEF1 lymphoid enhancer-binding factor 1
BC002865	0.0000004	MGC11242 hypothetical protein MGC11242
BF061965	0.0000011	KIAA1257 KIAA1257 protein
H05388	0.0000808	KIAA0844 KIAA0844 protein
AF243505	0.0002923	OTOR otoraplin
AL136721	p < 1e-07	DKFZP566K1946 hypothetical protein DKFZp566K1946
AK024715	p < 1e-07	FLJ21062 hypothetical protein FLJ21062
W52485	p < 1e-07	MST1 macrophage stimulating 1 (hepatocyte growth factor-like)
		CLECSEF1 C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 1. (cartilage-derived)
AA398015	0.0006358	CD22 CD22 antigen
NM_001771	p < 1e-07	ESTs
AW451965	p < 1e-07	ECM1 extracellular matrix protein 1
NM_004425	0.0000213	KIAA1010 KIAA1010 protein
AA962285	p < 1e-07	FLJ13187 phafin 2
BC011806	p < 1e-07	DGKD diacylglycerol kinase, delta (130KD)
AI304875	p < 1e-07	EPB41L4 erythrocyte protein band 4.1-like 4
AA406206	0.0000026	MGC11287 hypothetical protein MGC11287 similar to ribosomal protein S6 kinase ,
BC004540	0.0000031	MLLT2 myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2
L13773	p < 1e-07	FLJ23045 hypothetical protein FLJ23045
AK026698	p < 1e-07	G6PT1 glucose-6-phosphatase, transport (glucose-6-phosphate) protein 1
BC007617	p < 1e-07	EST
BF447022	0.0000008	

022041001010PC		
AL080136	0.0005363	SPAG6 sperm associated antigen 6
BC000691	p < 1e-07	LOC51673 brain specific protein
BF939249	p < 1e-07	ESTs
AF113212	0.0000001	MSTF032 MSTP032 protein
AI620139	p < 1e-07	ESTs
BC014336	0.0000002	HHEX hematopoietically expressed homeobox
AI241077	0.0001517	PAH phenylalanine hydroxylase
BC015571	p < 1e-07	SLC22A1L solute carrier family 22 (organic cation transporter), member 1-like
T23696	p < 1e-07	FLJ20015 hypothetical protein
AW196636	p < 1e-07	ESTs
R38689	0.0000006	PCL0 piccolo (presynaptic cytomatrix protein)
AJ251053	0.0000017	STHM sialyltransferase
BC002757	0.0000033	COX7A1 cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)
X59766	0.0000194	AZGP1 alpha-2-glycoprotein 1, zinc
AK000772	p < 1e-07	BA526D8.4 KRAB box containing C2H2 type zinc finger BA526D8.4
AW134884	0.0000014	GHRH growth hormone releasing hormone
AF263545	0.0000217	Homo sapiens HUT11 protein mRNA, partial 3' UTR
AF034996	0.0000879	AMPH amphiphysin (Stiff-Mann syndrome with breast cancer 128kD autoantigen)
NM_004029	p < 1e-07	IRF7 interferon regulatory factor 7
AI216751	0.0005965	ESTs
AI350518	p < 1e-07	ESTs
AL049329	p < 1e-07	DKFZP564G196 DKFZP564G196 protein
AK023757	p < 1e-07	Homo sapiens cDNA FLJ13695 fs, clone PLACE2000124
AI338252	p < 1e-07	LARGE like-glycosyltransferase
NM_005410	0.0001146	SEPP1 selenoprotein P, plasma, 1
AK024898	p < 1e-07	Homo sapiens cDNA: FLJ21245 fs, clone COL01184
AW207060	p < 1e-07	DNAJL1 hypothetical protein similar to mouse Dnajl1
AL136790	p < 1e-07	DKFZp434F1819 hypothetical protein DKFZp434F1819
AI973194	p < 1e-07	OVGP1 oviductal glycoprotein 1, 120kD (mucin 9, oviductin)
U01824	0.0000003	SLC1A2 solute carrier family 1 (glial high affinity glutamate transporter), member 2
AL136789	0.0000006	DKFZp434F1719 hypothetical protein DKFZp434F1719
BC014277	0.0000017	TIMP3 tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)
AK024750	0.0000299	C11orf14 chromosome 11 open reading frame 14
BC000187	0.0000002	COX6C cytochrome c oxidase subunit VIc

022041001010PC		
AB025904	p < 1e-07	CA14 carbonic anhydrase XIV
AW004703	0.0000002	FLJ10916 hypothetical protein FLJ10916
AK001865	0.0000065	Homo sapiens cDNA FLJ11003 fis, clone PLACE1002851
		Homo sapiens cDNA: FLJ23037 fis, clone LNG02036, highly similar to HSU68019 Homo sapiens mad protein
AK026690	p < 1e-07	homolog (hMAD-3) mRNA
BC001526	p < 1e-07	Homo sapiens, clone MGC:3245 IMAGE:3505639, mRNA, complete cds
BC014651	0.0000068	HOXB6 homeo box B6
AF085233	0.0000138	SGKL serum/glucocorticoid regulated kinase-like
AF000546	0.0000001	P2Y5 purinergic receptor (family A group 5)
AL109959	p < 1e-07	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1019273
R15800	p < 1e-07	ESTs
AW069800	0.0000002	Homo sapiens cDNA FLJ11685 fis, clone HEMBA1004934
AA906471	0.0000003	ESTs, Weakly similar to A28996 proline-rich protein M14 precursor - mouse [M.musculus]
AA233862	0.0000017	ESTs
AK056155	p < 1e-07	Homo sapiens cDNA FLJ31593 fis, clone NT2R12002481
AI214383	p < 1e-07	SYNGR1 synaptogyrin 1
AW070489	p < 1e-07	HOXC6 homeo box C6
AI401095	p < 1e-07	EST
AK027245	0.0000001	LOC55815 hypothetical protein
AW732240	0.0000024	ESTs
AF130068	0.0000027	SERPINA1 serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1
AA766862	p < 1e-07	KIAA0298 KIAA0298 gene product
AA765256	0.0000004	ESTs, Weakly similar to unnamed protein product [H.sapiens]
AA805317	0.0000038	HOXC4 homeo box C4
AF119815	0.0000147	GPR74 G protein-coupled receptor 74
X97881	p < 1e-07	GPRK2L G protein-coupled receptor kinase 2-like (Drosophila)
BF431989	0.0000001	ESTs
AI939560	p < 1e-07	ESTs, Weakly similar to CIKF_HUMAN VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 [H.sapiens]
AK024106	0.0000006	Homo sapiens cDNA FLJ14044 fis, clone HEMBA1006124
X95715	0.0000013	ABCC6 ATP-binding cassette, sub-family C (CFTR/MRP), member 6
AA409065	p < 1e-07	LEAP-2 liver-expressed antimicrobial peptide 2
AW590215	p < 1e-07	SLC4A8 solute carrier family 4, sodium bicarbonate cotransporter, member 8
BF508608	0.0000066	Homo sapiens cDNA FLJ12993 fis, clone NT2R3000197
BF508719	0.0006111	CGI-96 CGI-96 protein

022041001010PC		
AK023905	p < 1e-07	Homo sapiens cDNA FLJ13843 fis, clone THYRO1000796
AA631898	p < 1e-07	EST
AF030186	0.0001916	GPC4 glypican 4
AI655416	p < 1e-07	FLJ11756 hypothetical protein FLJ11756
BI492432	0.0000001	PMP22 peripheral myelin protein 22
AI273078	0.0000001	ELL2 ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR
BC011690	p < 1e-07	CORO2A coronin, actin binding protein, 2A
AI695809	p < 1e-07	A1BG alpha-1-B glycoprotein
AI753700	p < 1e-07	ESTs
AI567961	0.0000001	Homo sapiens cDNA FLJ13557 fis, clone PLACE1007737
AA053400	0.0000015	ESTs
AF182316	p < 1e-07	FER1L3 fer-1-like 3, myoferlin (C. elegans)
AI096474	0.0000001	APXL apical protein-like (Xenopus laevis)
BF475375	0.0000002	EST
AI125473	0.0000075	ESTs
NM_001900	0.0000093	CST5 cystatin D
AF173081	0.0006871	VELL1 Vertebrate LIN7 homolog 1, Tax interaction protein 33
AK024733	0.0000009	FLJ21080 hypothetical protein FLJ21080
AI341378	0.0000025	ESTs, Moderately similar to KIAA0940 protein [H.sapiens]
AF334710	0.0000246	Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence
AW073096	0.0001789	ESTs
AI373912	0.0005046	HABP2 hyaluronan binding protein 2
BC014949	p < 1e-07	LGP2 likely ortholog of mouse D111gp2
AA160784	p < 1e-07	ESTs
AL359558	0.0000013	Homo sapiens mRNA; cDNA DKFZp762O1615 (from clone DKFZp762O1615)
AI335013	0.0000015	Homo sapiens cDNA FLJ12052 fis, clone HEMBB1002042, moderately similar to CYTOCHROME P450 4C1 (EC 1.14.14.1)
AW138839	0.0000113	ESTs
RS4824	0.0001665	PCDH19 protocadherin 19
NS2765	0.0002372	CACNA1I calcium channel, voltage-dependent, alpha 1I subunit
AI571426	0.0006325	SFRP4 secreted frizzled-related protein 4
AI675370	0.0000005	Homo sapiens cDNA FLJ30279 fis, clone BRACE2002772, moderately similar to HYDROXYACYLGLUTATHIONE
AW452172	0.000098	HYDROLASE (EC 3.1.2.6)
		ESTs

BC001356	p < 1e-07	IFI35 interferon-induced protein 35
AK026642	0.0000001	C20orf35 chromosome 20 open reading frame 35
AL133102	0.0000012	CGI-142 CGI-142
AI950985	0.0000045	ESTs
BC002709	p < 1e-07	TP53TG1 TP53 target gene 1
BE465899	p < 1e-07	ESTs
AA905217	0.0000049	Homo sapiens cDNA FLJ25460 fis, clone TST09046
BC007659	0.0000091	NQO1 NAD(P)H dehydrogenase, quinone 1
M73481	p < 1e-07	GRPR gastrin-releasing peptide receptor
AI912080	p < 1e-07	ESTs
AF039698	p < 1e-07	SDCCAG33 serologically defined colon cancer antigen 33
AI668861	p < 1e-07	C18orf1 chromosome 18 open reading frame 1
AW139766	p < 1e-07	ESTs
AK000322	0.0000112	FLJ20315 hypothetical protein FLJ20315
R52665	0.0000001	KIAA0323 KIAA0323 protein
AY014282	0.0000008	FLJ12476 hypothetical protein FLJ12476
AF264784	p < 1e-07	TRPS1 trichorhinalphalangeal syndrome 1
AF073770	0.0000002	CROT carnitine O-octanoyltransferase
X08020	0.0000003	GSTM1 glutathione S-transferase M1
L03785	p < 1e-07	MYL5 myosin, light polypeptide 5, regulatory
AI651570	p < 1e-07	PCM1 pericentriolar material 1
AL049949	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp564L0822 (from clone DKFZp564L0822)
		Homo sapiens cDNA: FLJ23538 fis, clone LNG08010, highly similar to BETA2 Human MEN1 region clone
AK027191	0.0000008	epsilon/beta mRNA
AW450777	0.0000011	FLJ14009 hypothetical protein FLJ14009
AI027237	0.0000012	CACNA2D2 calcium channel, voltage-dependent, alpha 2/delta subunit 2
AA668884	0.0000034	ESTs
AL360254	0.0000007	SLI neuronal Shc adaptor homolog
BC014123	p < 1e-07	FLJ20920 hypothetical protein FLJ20920
AF334676	0.0001389	TEKT3 tektin 3
AI123176	p < 1e-07	ESTs
AK026782	p < 1e-07	FLJ23129 hypothetical protein FLJ23129
AF047033	0.0000008	SLC4A7 solute carrier family 4, sodium bicarbonate cotransporter, member 7
BF509554	0.0000021	ESTs

022041001010PC		
NM_001337	0.0003886	CX3CR1 chemokine (C-X3-C) receptor 1
AL353936	0.0004393	DKFZ761K1423 hypothetical protein DKFZp761K1423
AF285836	0.0000001	NPDC1 neural proliferation, differentiation and control, 1
AF038633	0.0000003	UCN urocortin
ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING		
AW301079	0.0006045	ENTRY [H.sapiens]
BF432086	0.0006733	LOC63923 hypothetical protein similar to tenascin-R
T52873	0.0000001	ESTs, Moderately similar to G02075 transcription repressor zinc finger protein 85 [H.sapiens]
AB018303	0.0000147	OAZ OLF-1/EBF associated zinc finger gene
AA233494	0.000036	ZNF132 zinc finger protein 132 (clone pHZ-12)
AK057894	0.0000335	Homo sapiens cDNA FLJ25165 fis, clone CBR08421
AF132197	p < 1e-07	PRO1331 hypothetical protein PRO1331
AL122071	0.0004254	Homo sapiens mRNA, cDNA DKFZp434H1235 (from clone DKFZp434H1235); partial cds
AK054617	0.0006328	Homo sapiens cDNA FLJ30055 fis, clone ADRGL1000165, weakly similar to IMIDAZOLONEPROPIONASE (EC 3.5.2.7)
AK024986	0.0000001	Homo sapiens cDNA: FLJ21333 fis, clone COL02535
L11672	0.0000009	ZNF91 zinc finger protein 91 (HPF7, HTF10)
Homo sapiens cDNA: FLJ21930 fis, clone HEP04301, highly similar to HSU90916 Human clone 23815 mRNA sequence		
AK025583	0.0000089	ESTs
R92436	0.0000707	AK5 adenylate kinase 5
AF062595	0.0002667	ACP5 acid phosphatase 5, tartrate resistant
AW575162	0.0000014	KIAA1881 KIAA1881 protein
AB067468	0.0000552	NPC1L1 NPC1 (Niemann-Pick disease, type C1, gene)-like 1
AF192522	0.0001271	Homo sapiens cDNA FLJ11648 fis, clone HEMBA1004405
AI668626	0.0000009	MVP major vault protein
NM_017458	p < 1e-07	DEFA DNA fragmentation factor, 45 kD, alpha polypeptide
AI93709	0.0000001	RPS27L ribosomal protein S27-like
BC003667	0.0000003	ESTs
BE857676	0.0004456	ESTs
AI910755	0.0000002	ESTs
Z48633	0.0000007	H.sapiens mRNA for retrotransposon
AK024192	0.0000001	Homo sapiens cDNA FLJ14130 fis, clone MAMMA1002618
L10386	0.0000027	TGM3 transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)
BC014105	0.0000005	LOC51015 CGI-111 protein

022041001010PC

H10298	0.000003	ESTs
AI620965	0.0000143	ESTs
BF056618	0.0002275	C20orf39 chromosome 20 open reading frame 39
AI984359	0.0000002	MAWBP MAWD binding protein
BC018001	0.0000004	MB myoglobin
AK026839	0.0000347	FLJ23186 hypothetical protein FLJ23186
BC012069	p < 1e-07	NUDT4 nudix (nucleoside diphosphate linked moiety X)-type motif 4
H66199	0.0000002	OR2W3P olfactory receptor, family 2, subfamily W, member 3 pseudogene
AL080213	0.0000003	Homo sapiens mRNA; cDNA DKFZp58611823 (from clone DKFZp58611823)
NM_030761	0.0000204	WNT4 wingless-type MMTV integration site family, member 4
AF052224	0.0000265	BSN bassoon (presynaptic cytomatrix protein)
NM_002625	0.0000553	PFKFB1 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1
AI741469	0.0000946	ESTs
AW293219	0.0004089	Homo sapiens cDNA FLJ12280 fis, clone MAMMA1001744
BC002752	0.0000008	PTD015 PTD015 protein
		Homo sapiens, Similar to hypothetical protein FLJ10761, clone MGC:19512 IMAGE:4329734, mRNA, complete cds
BC010082	0.0000028	BFSPP2 beaded filament structural protein 2, phakinin
AI954686	0.0001698	EST
AI620480	0.0003718	LOC51086 putative protein-tyrosine kinase
AA758546	0.0004796	CPE carboxypeptidase E
NM_001873	0.000995	NPHP1 nephronophthisis 1 (juvenile)
BC009789	0.0000001	FLJ13612 hypothetical protein FLJ13612
AF218006	0.0000018	EST
AA580186	0.0000046	ESTs
AI247211	0.0000002	MGC13038 hypothetical protein MGC13038
BC010117	0.0000006	CSF3R colony stimulating factor 3 receptor (granulocyte)
X55720	0.0000006	PTPN13 protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)
X79676	0.0000117	GSTT2 glutathione S-transferase theta 2
BC002415	0.0002872	PLIN1 perilipin
AI703322	0.0006439	COL12A1 collagen, type XII, alpha 1
NM_004370	0.0000819	KIAA0485 KIAA0485 protein
AW129056	0.0002021	DKFZP547L112 hypothetical protein DKFZp547L112
AL512723	0.0000013	CLST11240 CLST 11240 protein
AW613521	0.0000207	

022041001010PC		
AI280246	0.0000795	ESTs
AA827649	0.0000004	ESTs
AL161983	0.0000075	Homo sapiens mRNA; cDNA DKFZp761K2024 (from clone DKFZp761K2024)
AW453001	0.0006444	CEBPD CCAATenhancer binding protein (C/EBP), delta
AK025062	0.0000513	Homo sapiens cDNA: FLJ21409 fis, clone COL03924
H19223	0.0000011	ESTs, Weakly similar to Jc5238 galactosylceramide-like protein, GCP [H.sapiens]
BC011628	0.0000027	EPHX2 epoxide hydrolase 2, cytoplasmic
NM_007023	0.0000149	CAMP-GEFII cAMP-regulated guanine nucleotide exchange factor II
AI888490	0.0002268	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
AL133606	0.0000006	FLJ11142 hypothetical protein FLJ11142
AL096842	0.0000008	ATIP1 AT2 receptor-interacting protein 1
AW301074	0.0000056	ESTs, Weakly similar to GTXH_HUMAN GLUTATHIONE-S-TRANSFERASE HOMOLO [H.sapiens]
AF131794	0.0004664	KIAA0378 KIAA0878 protein
AI499501	0.0001437	ESTs, Weakly similar to FIMOD_HUMAN FIBROMODULIN PRECURSOR [H.sapiens]
AF002672	0.0002138	LOH11CR2A loss of heterozygosity, 11, chromosomal region 2, gene A
AK000785	0.0000103	FLJ20778 epsin 3
AW183685	0.0000151	ESTs
BC017422	0.0000003	Homo sapiens, clone MGC:27375 IMAGE:4688423, mRNA, complete cds
BE501103	0.0000003	Homo sapiens cDNA FLJ32173 fis, clone PLACE6000953
BC005066	0.0000003	Homo sapiens, clone IMAGE:3347954, mRNA, partial cds
BC006534	0.0000028	SARCOSIN sarcomeric muscle protein
AI800042	0.000004	ESTs
AB062787	0.0000042	TREM2 triggering receptor expressed on myeloid cells 2
NM_001197	0.0000451	BIK BCL2-interacting killer (apoptosis-inducing)
BC013151	0.0000006	Homo sapiens, Similar to FIKEN cDNA 4933433C09 gene, clone MGC:21628 IMAGE:4385421, mRNA, complete cds
BC001314	0.0000018	Homo sapiens, Similar to clone FLB3816, clone IMAGE:3454380, mRNA
BC000006	0.0000506	ATP1B1 ATPase, Na ⁺ /K ⁺ transporting, beta 1 polypeptide
R63503	0.0000015	ESTs
AI733491	0.0000215	ESTs
BC009753	0.0000598	Homo sapiens, clone IMAGE:3833472, mRNA
BC008857	0.0000022	NFATC4 nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4
S77873	0.0000023	CYP2E cytochrome P450, subfamily IIE (ethanol-inducible)
AF131833	0.0003466	LOC57795 hypothetical protein from clone 24828

AF101477	0.0004668	GNMT glycine N-methyltransferase
AA708035	0.0005873	ESTs
BC005997	0.0000003	MGC14801 hypothetical protein MGC14801
BE501474	0.000001	Homo sapiens mRNA; cDNA DKFZp434P182 (from clone DKFZp434P182)
A1499593	0.0000015	IRX5 iroquois homeobox protein 5
AW136984	0.0000906	FLJ11235 hypothetical protein
BC007808	0.000002	MYH7B myosin, heavy polypeptide 7B, cardiac muscle, beta
A1311127	0.0000065	ESTs
AF094754	0.0000257	GLRB glycine receptor, beta
AW118445	0.0000387	CELSR2 cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)
AL136678	0.0000276	FLJ12428 hypothetical protein FLJ12428
A1733703	0.0004539	ESTs
AK025915	0.0000003	Homo sapiens cDNA FLJ10728 fis, clone NT2RP3001236
AW205835	0.0000026	ESTs
A1205008	0.0000041	SLC1A4 solute carrier family 1 (glutamate/neutral amino acid transporter), member 4
AL161993	0.0000451	LOC57168 similar to aspartate beta hydroxylase (ASPH)
NM_013267	0.00005	GA breast cell glutaminase
AA758934	0.000002	Homo sapiens cDNA FLJ13362 fis, clone PLACE1000236
BC015947	0.0001039	KCNBS3 potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3
AF226730	0.0003918	Cyt19 Cyt19 protein
AW139590	0.0002061	KIAA1443 KIAA1443 protein
NM_005906	0.0003675	MAK male germ cell-associated kinase
BC005124	0.0008792	HOXD3 homeo box D3
A1922007	0.0000011	ESTs
AW082270	0.0000015	ESTs, highly similar to AC004836.1 similar to cadherin and Drosophila Fat protein [H.sapiens]
AY014284	0.0000449	TSGA10 testis specific, 10
AJ406933	0.0001677	KAP3.3 keratin associated protein 3.3
AW470748	0.0000153	BCAR3 breast cancer anti-estrogen resistance 3
U06641	0.0000758	UGT2B15 UDP glycosyltransferase 2 family, polypeptide B15
A1658924	0.0006314	EST
BC002689	0.0000016	GLA galactosidase, alpha
AF023676	0.000007	TM7SF2 transmembrane 7 superfamily member 2
BC001109	0.0001481	CRABP2 cellular retinoic acid binding protein 2
BC000897	0.0005356	IFITM1 interferon induced transmembrane protein 1 (9-27)

022041001010PC

BC017703	0.0002482	LRRFP2 leucine rich repeat (in FLI) interacting protein 2
BF436849	0.0000019	ESTs
AV661191	0.0000777	PDCD4 programmed cell death 4 (neoplastic transformation inhibitor)
BC015657	0.0004846	OAI ocular albinism 1 (Netherlands-Falls)
N94443	0.0006496	KIAA0802 KIAA0802 protein
AK025431	0.0000008	Homo sapiens cDNA: FLJ21778 fis, clone HEP00201
AF016267	0.0000016	TNFRSF10C tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain
AF297872	0.0000004	TREP-132 transcriptional regulating protein 132
BC003180	0.0000047	SNRPN small nuclear ribonucleoprotein polypeptide N
AI804733	0.0000051	Homo sapiens cDNA FLJ33322 fis, clone PROST2003577
AI026838	0.0000127	ESTs, Weakly similar to NUCL_HUMAN NUCLEOLIN [H.sapiens]
AI097422	0.0000658	LOC57100 organic cation transporter
AA912183	0.0005194	ESTs
AI399698	0.0000126	EST
AI272951	0.0000286	SERPINC1 serine (or cysteine) proteinase inhibitor, clade C (antithrombin), member 1
AW448954	0.0000899	FLJ14871 hypothetical protein FLJ14871
AK027207	0.0007043	FLJ23554 hypothetical protein FLJ23554
BC010691	0.0000064	MGC9564 similar to RIKEN cDNA 1110002C08 gene
BC011973	0.0000109	FLJ20505 hypothetical protein FLJ20605
AW341854	0.000012	SPAG8 sperm associated antigen 8
BC014456	0.0006392	CHRNA6 cholinergic receptor, nicotinic, alpha polypeptide 6
AF037070	0.0000154	KIAA0464 ligand of neuronal nitric oxide synthase with carboxyl-terminal PDZ domain
BC007373	0.0000041	MGC16179 hypothetical protein MGC16179
BC010690	0.0003139	FLJ14529 hypothetical protein FLJ14529
AI740671	0.0003413	Homo sapiens cDNA FLJ32430 fis, clone SKMUS2001129, weakly similar to NAD-DEPENDENT METHANOL
AI199647	0.0000028	DEHYDROGENASE (EC 1.1.1.244)
AI659491	0.0000053	SCNN1D sodium channel, nonvoltage-gated 1, delta
AA854341	0.0000092	EST
NM_005677	0.0000028	Homo sapiens cDNA FLJ12924 fis, clone NT2RP2004709
AK057782	0.000412	COLQ collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase
AL080078	0.0000036	Homo sapiens cDNA FLJ25053 fis, clone CBL04266
AI434326	0.0004414	Homo sapiens mRNA: cDNA DKFZ564D1462 (from clone DKFZ564D1462)
AF331643	0.0000005	ATP2A3 ATPase, Ca++ transporting, ubiquitous
		Homo sapiens chromosome 17 open reading frame 26 (C17orf26) mRNA, complete cds

022041001010PC		
BC007438	0.0000058	MGC4251 hypothetical protein MGC4251
AA555036	0.0000147	SORD sorbitol dehydrogenase
AK021467	0.0000544	Homo sapiens cDNA FLJ11405 fis, clone HEMBA1000769
BF001174	0.0000709	CAP2 adenyl cyclase-associated protein 2
AL136680	0.0004515	Homo sapiens mRNA; cDNA DKFZp564C2478 (from clone DKFZp564C2478); complete cds
AL110174	0.0005604	STMN2 stathmin-like 2
AK026288	0.0004417	FLJ22635 hypothetical protein FLJ22635
NM_003512	0.0005828	H2AFL H2A histone family, member L
AW070686	0.000002	ESTs
BC000866	0.0000034	TIMP1 tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)
AF070555	0.0000131	PRSS1 protease, serine, 11 (IGF binding)
AI962213	0.0001497	KIAA0705 atrophin-1 interacting protein 1; activin receptor interacting protein 1
AW419319	0.0008904	ODZ2 odd Oz/ten-m homolog 2 (Drosophila, mouse)
N70848	0.0000023	ESTs, Moderately similar to I38022 hypothetical protein [H.sapiens]
NM_001773	0.0009366	CD34 CD34 antigen
AK026301	0.0009911	Homo sapiens cDNA: FLJ22648 fis, clone HSI07329
F10094	0.0000158	ESTs
AK055747	0.0007753	FLJ13236 hypothetical protein FLJ13236
A1797308	0.0000092	ESTs, Weakly similar to alternatively spliced product using exon 13A [H.sapiens]
AA746504	0.0000207	Homo sapiens cDNA FLJ30188 fis, clone BRACE2001267
AK025307	0.0000623	CPT1A carnitine palmitoyltransferase I, liver
BC005357	0.0000049	MGC12458 hypothetical protein MGC12458
U31214	0.0000475	FXYD3 FXYP domain-containing ion transport regulator 3
AW243677	0.00001	FLJ22457 hypothetical protein FLJ22457
AI868636	0.0001498	Homo sapiens cDNA FLJ30403 fis, clone BRACE2008480
AI659877	0.0008135	ESTs
AK025627	0.0000049	Homo sapiens, clone IMAGE:3937015, mRNA, partial cds
AI811067	0.0000149	Homo sapiens cDNA FLJ31422 fis, clone NT2NE200384, weakly similar to MICRONUCLEAR LINKER HISTONE
AW139902	0.0002142	POLYPROTEIN
AB020711	0.0008427	ESTs
AW339037	0.0000243	KIAA0904 KIAA0904 protein
AV647264	0.0000324	ESTs
AI002941	0.0000063	ESTs
		Human glucose transporter pseudogene

022041001010PC		
BC017073	0.0007021	Homo sapiens, Similar to RIKEN cDNA 1810054O13 gene, clone IMAGE:3845933, mRNA, partial cds
AW102641	0.0000112	ESTs
AK000341	0.0000133	ELOVL2 elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2
NM_030878	0.0007446	CYP2C8 cytochrome P450, subfamily 11C (mephenytoin 4-hydroxylase), polypeptide 8
AF288399	0.0000055	C1orf25 chromosome 1 open reading frame 25
BC005956	0.0000248	RLN1 relaxin 1 (H1)
D50419	0.0000877	ZNF175 zinc finger protein 175
AK025905	0.0002948	SOX17 SRY-related HMG-box transcription factor SOX17
AK026760	0.0000265	C20orf119 chromosome 20 open reading frame 119
AA999861	0.0001219	ESTs
AA883836	0.0003305	ESTs, Weakly similar to CGHUTL collagen alpha 1(III) chain precursor [H.sapiens]
AJ420485	0.0000088	MRPL33 mitochondrial ribosomal protein L33
BF511682	0.0004053	SH2 hematopoietic SH2 protein
M59303	0.0000685	PROZ protein Z, vitamin K-dependent plasma glycoprotein
BM127823	0.0001431	KIAA1917 KIAA1917 protein
U60975	0.0002497	SORL1 sortilin-related receptor, L(DLR class) A repeats-containing
AA659779	0.0000288	ESTs
BC006289	0.0000416	FLJ11151 hypothetical protein FLJ11151
AF059321	0.0000839	SIAT4A sialyltransferase 4A (beta-galactosidase alpha-2,3-sialyltransferase)
N59238	0.0000132	DKFZp761O0113 hypothetical protein DKFZp761O0113
AB032417	0.0003999	FZD4 frizzled homolog 4 (Drosophila)
L13220	0.0009771	CALB3 calbindin 3, (vitamin D-dependent calcium binding protein)
AI085836	0.0000535	ESTs, Weakly similar to F5HU22 ribosomal protein L17, cytosolic [H.sapiens]
AI492117	0.0001096	Homo sapiens putative ion channel protein CATSPER2 (CATSPER2), mRNA
AI311775	0.0001113	ESTs
AW295401	0.0005407	FLJ10647 hypothetical protein FLJ10647
BC013107	0.0000099	H326 H326
BC000566	0.0000109	RAYL putative GTP-binding protein similar to RAY/RAB1C
AA149305	0.0005606	ITGBL1 integrin, beta-like 1 (with EGF-like repeat domains)
AK025757	0.0000282	FLJ22104 hypothetical protein FLJ22104
AW070798	0.0000334	EST
BE549691	0.0000361	Homo sapiens cDNA FLJ30927 fis, clone FEBRA2006736
AI475953	0.0000816	ESTs
AK026438	0.0000114	Homo sapiens cDNA: FLJ22785 fis, clone KAI/A2081

022041001010PC		
AL161961	0.0000246	KIAA1554 KIAA1554 protein
AF242557	0.0001086	TSCOT thymic stromal co-transporter
BC016628	0.0000127	DKFZP434D146 DKFZP434D146 protein
AA761787	0.0000158	ESTs
BE670572	0.0009122	ESTs
BC006131	0.0000961	MGC13047 hypothetical protein MGC13047
AF024690	0.0002962	GPR43 G protein-coupled receptor 43
AI961887	0.0007391	COL3A1 collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)
BC004471	0.0000513	APM2 adipose specific 2
AK000542	0.0000616	FLJ20535 hypothetical protein FLJ20535
BC010652	0.0000856	MGC9753 hypothetical gene MGC9753
AI859284	0.0001958	ESTs, Weakly similar to T42709 hypothetical protein DKFZp58610821.1 [H.sapiens]
BC005364	0.0000764	FLJ11218 hypothetical protein FLJ11218
AI732388	0.0003354	MGAT14A mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isoenzyme A
AI248610	0.0000466	ESTs
AK026720	0.0001708	Homo sapiens cDNA: FLJ23067 fis, clone LNG04993
NM_000609	0.0008601	SDF1 stromal cell-derived factor 1
NM_006713	0.000127	PC4 activated RNA polymerase II transcription cofactor 4
AK054839	0.0001666	Homo sapiens cDNA FLJ30277 fis, clone BRACE2002752
AI087975	0.0001916	ESTs
AF220030	0.0002753	TRIM6 tripartite motif-containing 6
BC000632	0.0000354	S100A13 S100 calcium binding protein A13
BC015613	0.0001785	GATA2 GATA binding protein 2
AA603977	0.000372	KLK4 kallikrein 4 (protease, enamel matrix, prostate)
AW197863	0.0000468	ESTs
BM127867	0.0000528	MDM1 nuclear protein double minute 1
AA830549	0.0003809	VAMP1 vesicle-associated membrane protein 1 (synaptobrevin 1)
BF477905	0.0005735	ESTs
R45048	0.0001759	C22orf1 chromosome 22 open reading frame 1
AB033110	0.0001596	KIAA1284 KIAA1284 protein
AW293849	0.0001623	ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]
BC014117	0.0002492	TBXAS1 thromboxane A synthase 1 (platelet, cytochrome P450, subfamily V)
AK022060	0.0005048	Homo sapiens cDNA FLJ11998 fis, clone HEMBB1001521
AA806859	0.0007266	FLJ14281 hypothetical protein FLJ14281

022041001010PC

AW291180	0.0000866	ADORA3 adenosine A3 receptor
BF510778	0.0001368	ESTs
AA603743	0.0002352	EST
BC005305	0.0006323	COL4A6 collagen, type IV, alpha 6
AF068180	0.0001499	BLNK B-cell linker
R46824	0.0002785	SRGAP3 KIAA0411 gene product
AI081593	0.0001534	ESTs
AF311325	0.0001578	GPD2 glycerol-3-phosphate dehydrogenase 2 (mitochondrial)
AK055280	0.0001954	Homo sapiens cDNA FLJ30718 fts, clone FCBBF2001675
AB018316	0.0006996	KIAA0773 KIAA0773 gene product
AK025168	0.0000869	OSBPL6 oxysterol binding protein-like 6
AL117616	0.0001068	SRI sorcin
AF332975	0.0005447	ZAN zonadhesin
R43793	0.0001576	HSPA1L heat shock 70kD protein 1-like
AI307801	0.000302	KIAA1072 KIAA1072 protein
AK027036	0.0008803	RU2 RU2S
BC006378	0.0001365	UBE1L ubiquitin-activating enzyme E1-like
AL137559	0.0004641	PCANAP7 prostate cancer associated protein 7
J03607	0.0001134	KRT19 keratin 19
N93663	0.0003213	ESTs
AA767639	0.0006013	KIAA0227 KIAA0227 protein
BF448987	0.0002835	ESTs
AL110131	0.0006287	KIAA1223 KIAA1223 protein
NM_006455	0.0001119	SC65 nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein
R56793	0.0009148	AGXT2L1 alanine-glyoxylate aminotransferase 2-like 1
AF059617	0.0006528	SNK serum-inducible kinase
BC005055	0.0003206	FOXPI1 forkhead box P1
AF141332	0.0004598	APOB48R apolipoprotein B48 receptor
AK025772	0.0001313	Homo sapiens cDNA: FLJ22119 fts, clone HEP18852
AI424409	0.0002138	ESTs, highly similar to LB4D_HUMAN NADP-DEPENDENT LEUKOTRIENE B4 12-
AK056154	0.0007347	HYDROXYDEHYDROGENASE [H.sapiens]
BC014533	0.0001558	Homo sapiens cDNA FLJ31592 fts, clone NT2R12002447
AI089428	0.0007681	MEF-2 myelin gene expression factor 2
		ESTs

022041001010PC

BC017411	0.0001941	Homo sapiens, clone IMAGE:4618419, mRNA, partial cds
AF263462	0.0003563	CGN cingulin
BC003608	0.0005011	RBPMS RNA-binding protein gene with multiple splicing
AK027146	0.0004053	RPL5 ribosomal protein L5
U90914	0.0009563	CPD carboxypeptidase D
BF508058	0.0002228	DKFZP564D166 putative ankyrin-repeat containing protein
AK026256	0.0007805	MGC4171 hypothetical protein MGC4171
AB069698	0.0005545	ADAMTS13 a disintegrin-like and metalloprotease (repolysin type) with thrombospondin type 1 motif, 13
BC005359	0.0002707	GMFB glia maturation factor, beta
NM_021194	0.0002725	SLC30A1 solute carrier family 30 (zinc transporter), member 1
AI311898	0.0003307	ESTs
NM_002538	0.0005858	OCLN occludin
AF222340	0.0007234	ARTS-1 type 1 tumor necrosis factor receptor shedding aminopeptidase regulator
W32171	0.0005402	Homo sapiens cDNA FLJ13613 fis, clone PLACE1010856
BC009869	0.0008215	SERF2 small EDRK-rich factor 2
AK021674	0.0003543	Homo sapiens cDNA FLJ11612 fis, clone HEMBA1004011
AB039903	0.0007986	TRIM34 tripartite motif-containing 34
AJ252236	0.0004879	CAMK2B calcium/calmodulin-dependent protein kinase (CaM kinase) II beta
BC002745	0.0006025	ENO2 enolase 2, (gamma, neuronal)
BE349538	0.000829	TM7SF1 transmembrane 7 superfamily member 1 (upregulated in kidney)
NM_014583	0.0009047	LMCD1 LIM and cysteine-rich domains 1
AL046192	0.0004687	PVT1 Pvt1 oncogene homolog, MYC activator (mouse)
AK023312	0.0008557	Homo sapiens cDNA FLJ13250 fis, clone OVARC1000724
AF054181	0.0007103	NDUFB1 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1 (7kD, MNLL)
AI268717	0.000927	ESTs, Highly similar to AC004836 1 similar to cadherin and Drosophila Fat protein [H.sapiens]
AI733236	0.000961	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]

Table 4. Genes that are overexpressed in ER negative cells, and underexpressed in ER positive cells

GeneID	P-value	Description
NM_014211	p < 1e-07	GABRP gamma-aminobutyric acid (GABA) A receptor, pi
BC017913	p < 1e-07	ART3 ADP-ribosyltransferase 3
H29323	p < 1e-07	SFRP1 secreted frizzled-related protein 1
AW192480	p < 1e-07	SLC6A14 solute carrier family 6 (neurotransmitter transporter), member 14
AI332979	p < 1e-07	KCNKG1 potassium voltage-gated channel, subfamily G, member 1
AI404611	p < 1e-07	BCL11A B-cell CLL/lymphoma 11A (zinc finger protein)
		Homo sapiens cDNA FLJ11796 fis, clone HEMBA1006158, highly similar to Homo sapiens transcription factor
AW139831	p < 1e-07	forkhead-like 7 (FKHL7) gene
BC008484	p < 1e-07	DKFZF564D206 DKFZF564D206 protein
BC014152	p < 1e-07	KRT6A keratin 6A
BC000045	p < 1e-07	TONDU1 TONDU
AB028641	p < 1e-07	SOX11 SRY (sex determining region Y)-box 11
AA452915	p < 1e-07	EN1 engrailed homolog 1
AI367357	p < 1e-07	ESTs
U95089	p < 1e-07	EGFR epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
NM_001453	p < 1e-07	FOXC1 forkhead box C1
AW136298	p < 1e-07	E48 lymphocyte antigen 6 complex, locus D
AI358916	p < 1e-07	ZIC1 Zinc family member 1 (odd-paired homolog, Drosophila)
BC015525	p < 1e-07	KLK6 kallikrein 6 (neurosin, zyme)
BC012089	p < 1e-07	PROM1.1 prominin-like 1 (mouse)
AW004032	p < 1e-07	LOC56963 hypothetical protein from EUROIMAGE 363668
AF084830	p < 1e-07	KCNK5 potassium channel, subfamily K, member 5 (TASK-2)
AW450675	p < 1e-07	ESTs
AA452928	p < 1e-07	GPR51 G protein-coupled receptor 51
AF308297	p < 1e-07	PPP1R14C protein phosphatase 1, regulatory (inhibitor) subunit 14C
NM_003508	p < 1e-07	FZD9 frizzled homolog 9 (Drosophila)
AW291189	p < 1e-07	ESTs
BC012299	p < 1e-07	FABP7 fatty acid binding protein 7, brain
BC005910	p < 1e-07	MIA melanoma inhibitory activity
AA609183	p < 1e-07	ESTs

Z73678	p < 1e-07	PKP1 plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)
BC007008	p < 1e-07	CRYAB crystallin, alpha B
NM_032047	p < 1e-07	B3GNT5 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5
AY029179	p < 1e-07	JPO1 c-Myc target JPO1
AF055982	p < 1e-07	KLK8 kallikrein 8 (neuropsin/ovasin)
AI160174	p < 1e-07	ESTs
AF257472	p < 1e-07	C21orf68 chromosome 21 open reading frame 68
R50991	p < 1e-07	FLJ11413 hypothetical protein FLJ11413
AK025066	p < 1e-07	FLJ10901 hypothetical protein FLJ10901
BC003628	p < 1e-07	HBP17 heparin-binding growth factor binding protein
AI279525	p < 1e-07	ELF5 E74-like factor 5 (ets domain transcription factor)
NM_024423	p < 1e-07	DSC3 desmocollin 3
BC007394	p < 1e-07	MGC16291 hypothetical protein MGC16291
AK026818	p < 1e-07	Homo sapiens cDNA: FLJ23165 fs, clone LNG09846
AA521195	p < 1e-07	LAMP3 lysosomal-associated membrane protein 3
AA156097	p < 1e-07	ESTs, Weakly similar to LKHU proteoglycan link protein precursor [H.sapiens]
AW137881	p < 1e-07	RARRES1 retinoic acid receptor responder (tazarotene induced) 1
BC014941	p < 1e-07	ID4 inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
AA622986	p < 1e-07	ESTs
AA922144	p < 1e-07	AQP5 aquaporin 5
AI800206	p < 1e-07	STAC src homology three (SH3) and cysteine rich domain
NM_002964	p < 1e-07	S100A8 S100 calcium binding protein A8 (calgranulin A)
BC007595	p < 1e-07	SOX10 SRY (sex determining region Y)-box 10
AK000442	p < 1e-07	FLJ20435 hypothetical protein FLJ20435
BC017352	p < 1e-07	TRIM29 tripartite motif-containing 29
AJ000388	p < 1e-07	CAPN6 calpain 6
AL137311	p < 1e-07	Homo sapiens mRNA: cDNA DKFZp761G02121 (from clone DKFZp761G02121); partial cds
BC012914	p < 1e-07	Homo sapiens cDNA FLJ31360 fs, clone MESAN2000572
AA194943	p < 1e-07	DEFB1 defensin, beta 1
AL110178	p < 1e-07	TRIM2 tripartite motif-containing 2
AW204371	p < 1e-07	DSC2 desmocollin 2
AI049783	p < 1e-07	ESTs
BC000183	p < 1e-07	TMSNB thymosin, beta, identified in neuroblastoma cells
BI495988	p < 1e-07	MET met proto-oncogene (hepatocyte growth factor receptor)

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AL110126	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone DKFZp564H1916)
AW140023	p < 1e-07	FLJ13204 hypothetical protein FLJ13204
BC003635	p < 1e-07	MMP7 matrix metalloproteinase 7 (matrilysin, uterine)
BC016004	p < 1e-07	MARCO macrophage receptor with collagenous structure
AW264415	p < 1e-07	Homo sapiens, clone MGC:24011 IMAGE:4091916, mRNA, complete cds
AI375448	p < 1e-07	GPM6E glycoprotein M6B
N64339	p < 1e-07	GJB6 gap junction protein, beta 6 (connexin 30)
AK026420	p < 1e-07	DMN desmuslin
BF433019	p < 1e-07	ESTs, Weakly similar to TRHY_HUMAN TRICHOHYAL [H.sapiens]
AI885044	p < 1e-07	KIT v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
AK021785	p < 1e-07	Homo sapiens cDNA FLJ11723 fis, clone HEMBA1005314
AF089854	p < 1e-07	TU3A TU3A protein
AF033021	p < 1e-07	KCNM4 potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4
AI948466	p < 1e-07	INDO indoleamine-pyrrole 2,3 dioxygenase
AW291290	p < 1e-07	ESTs
AF052117	p < 1e-07	Homo sapiens clone 23809 mRNA sequence
NM_002965	p < 1e-07	S100A9 S100 calcium binding protein A9 (calgranulin B)
NM_006522	p < 1e-07	WNT6 wingless-type MMTV integration site family, member 6
U17077	p < 1e-07	BENE BENE protein
AW449979	p < 1e-07	SLC15A1 solute carrier family 15 (oligopeptide transporter), member 1
NM_001793	p < 1e-07	CDH3 cadherin 3, type 1, P-cadherin (placental)
AY035400	p < 1e-07	PCOLCE2 procollagen C-endopeptidase enhancer 2
AF047348	p < 1e-07	APBA2 amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like)
AI732309	p < 1e-07	EPHB1 EphB1
AA584033	p < 1e-07	KRT6B keratin 6B
NM_002639	p < 1e-07	SERPINB5 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 5
BC000332	p < 1e-07	UCHL1 ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
BF224381	p < 1e-07	ESTs
BC017583	p < 1e-07	SCRG1 scrapie responsive protein 1
NM_004961	p < 1e-07	GABRE gamma-aminobutyric acid (GABA) A receptor, epsilon
AI351524	p < 1e-07	DMD dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206,
BC001283	p < 1e-07	DXS230, DXS239, DXS268, DXS269, DXS270, DXS272
BC004376	p < 1e-07	NFIB nuclear factor I/B
		ANXA8 annexin A8

022041001010PC		
AB037813	p < 1e-07	DKFZp762K222 hypothetical protein DKFZp762K222
AK024990	p < 1e-07	PPARGC1 peroxisome proliferative activated receptor, gamma, coactivator 1
AF241254	p < 1e-07	ACE2 angiotensin I converting enzyme (peptidyl-dipeptidase A) 2
AI800677	p < 1e-07	SLP1 secretory leukocyte protease inhibitor (antileukoproteinase)
BC012908	p < 1e-07	NMU neuromedin U
BC012097	p < 1e-07	OCA2 oculocutaneous albinism II (pink-eye dilution homolog, mouse)
R44714	p < 1e-07	Homo sapiens cDNA FLJ13136 fis, clone NT2RP3003139
R15881	p < 1e-07	CHRM3 cholinergic receptor, muscarinic 3
AK025909	p < 1e-07	Homo sapiens cDNA: FLJ22256 fis, clone HRC02860
AI754805	p < 1e-07	SMOC1 secreted modular calcium-binding protein 1
BC009581	p < 1e-07	HSD17B2 hydroxysteroid (17-beta) dehydrogenase 2
X59770	p < 1e-07	IL1R2 interleukin 1 receptor, type II
M76482	p < 1e-07	DSG3 desmoglein 3 (pemphigus vulgaris antigen)
AI368024	p < 1e-07	ESTs
BC015753	p < 1e-07	GRO2 GRO2 oncogene
BC014950	p < 1e-07	CA9 carbonic anhydrase IX
BC008366	p < 1e-07	DDC dopa decarboxylase (aromatic L-amino acid decarboxylase)
AI970748	p < 1e-07	ESTs
BC001766	p < 1e-07	S100B S100 calcium binding protein, beta (neural)
AW206460	p < 1e-07	KIAA0481 KIAA0481 gene product
AF361486	p < 1e-07	MUC16 mucin 16
BC000992	p < 1e-07	CSRP2 cysteine and glycine-rich protein 2
AI202593	p < 1e-07	CYP7B1 cytochrome P450, subfamily VIIb (oysterol 7 alpha-hydroxylase), polypeptide 1
NM_006115	p < 1e-07	PRAME preferentially expressed antigen in melanoma
BC011976	p < 1e-07	GRO1 GRO1 oncogene (melanoma growth stimulating activity, alpha)
BC006226	p < 1e-07	DLX5 distal-less homeo box 5
AL137289	p < 1e-07	ARHGEF4 Rho guanine nucleotide exchange factor (GEF) 4
BC005083	p < 1e-07	MGC13057 hypothetical protein MGC13057
AI261967	p < 1e-07	ADORA2B adenosine A2b receptor
AI273928	p < 1e-07	ALDH1A3 aldehyde dehydrogenase 1 family, member A3
BC005948	p < 1e-07	SMPX small muscle protein, X-linked
NM_006769	p < 1e-07	LMO4 LIM domain only 4
AL117452	p < 1e-07	DKFZP586G1517 DKFZP586G1517 protein
AA587049	p < 1e-07	PLA2G4A phospholipase A2, group IVA (cytosolic, calcium-dependent)

AI804716	p < 1e-07	ESTs
AI637899	p < 1e-07	GAL galanin
AF269101	p < 1e-07	MID1 midline 1 (Opitz/BBB syndrome)
NM_003034	p < 1e-07	SIAT8A sialyltransferase 8A (alpha-N-acetylneuraminate: alpha-2,8-sialyltransferase, GD3 synthase)
AF141339	p < 1e-07	DKFZP564D0764 DKFZP564D0764 protein
AI095049	p < 1e-07	Homo sapiens cDNA FLJ31627 fis, clone NT2RI2003338
AI498405	p < 1e-07	ESTs, Weakly similar to B43647 GTP-binding protein rab8 [H.sapiens]
AF130728	p < 1e-07	DMRT1 doublesex and mab-3 related transcription factor 1
AVW206700	p < 1e-07	KLK7 kallikrein 7 (chymotryptic, stratum corneum)
AB042405	p < 1e-07	MLZE melanoma-derived leucine zipper, extra-nuclear factor
AF104032	p < 1e-07	SLC7A5 solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
AA521486	p < 1e-07	CECR7 cat eye syndrome chromosome region, candidate 7
AI024603	p < 1e-07	HAP1P huntingtin-associated protein interacting protein (duo)
AI830532	p < 1e-07	ESTs
M57892	p < 1e-07	CA6 carbonic anhydrase VI
NM_003914	p < 1e-07	CCNA1 cyclin A1
S72493	p < 1e-07	KRT16 keratin 16 (focal non-epidermolytic palmoplantar keratoderma)
NM_004938	p < 1e-07	DAPK1 death-associated protein kinase 1
AW071804	p < 1e-07	ESTs
NM_002996	p < 1e-07	SCYD1 small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)
NM_002299	p < 1e-07	LCT lactase
R55787	p < 1e-07	KIAA1069 KIAA1069 protein
AF271781	p < 1e-07	ITM3 integral membrane protein 3
AA716090	p < 1e-07	BOC brother of CDO
AI420468	p < 1e-07	KIAA1209 KIAA1209 protein
H09748	p < 1e-07	BCL11B B-cell CLL/lymphoma 11B (zinc finger protein)
AA806280	p < 1e-07	Homo sapiens cDNA FLJ31951 fis, clone NT2RP7007177, weakly similar to Homo sapiens multiple membrane spanning receptor TRC8 mRNA
BI492630	p < 1e-07	SLC9A6 solute carrier family 9 (sodium/hydrogen exchanger), isoform 6
BC004397	p < 1e-07	MGC10381 hypothetical protein MGC10381
AF095719	p < 1e-07	CPA4 carboxypeptidase A4
AF331525	p < 1e-07	SLC26A9 solute carrier family 26, member 9
R38090	p < 1e-07	G2 G2 protein
AF117108	p < 1e-07	KOC1 IGF-II mRNA-binding protein 3

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AF127563	p < 1e-07	DKK1 dickkopf homolog 1 (Xenopus laevis)
AA633482	p < 1e-07	EST
BC008588	p < 1e-07	PLS3 plastin 3 (T isoform)
NM_002852	p < 1e-07	PTX3 pentaxin-related gene, rapidly induced by IL-1 beta
AF123074	p < 1e-07	DNC1 dynein, cytoplasmic, intermediate polypeptide 1
AK000123	p < 1e-07	C20orf42 chromosome 20 open reading frame 42
AW444437	0.000001	ESTs
AI557322	p < 1e-07	ESTs
AB053450	p < 1e-07	KIAA1776 fibrillin3
X53578	p < 1e-07	FUT3 fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group included)
AF043473	p < 1e-07	KCNS1 potassium voltage-gated channel, delayed-rectifier, subfamily S, member 1
AF197137	p < 1e-07	FN5 FN5 protein
BC017733	p < 1e-07	MRAS muscle RAS oncogene homolog
AW265625	p < 1e-07	ESTs
AA527072	p < 1e-07	EST
BC016666	p < 1e-07	Homo sapiens, clone IMAGE:3917693, mRNA
AF220183	p < 1e-07	HT009 uncharacterized hypothalamus protein HT009
AI356375	p < 1e-07	CDKN2A cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)
AW780208	p < 1e-07	Homo sapiens, clone MGC:15887 IMAGE:3530481, mRNA, complete cds
BC006097	p < 1e-07	HLA-DOB major histocompatibility complex, class II, DO beta
AI740531	p < 1e-07	MAPK4 mitogen-activated protein kinase 4
L20433	p < 1e-07	POU4F1 POU domain, class 4, transcription factor 1
NM_003806	p < 1e-07	HRK harakiri, BCL2 interacting protein (contains only BH3 domain)
BC007541	p < 1e-07	MGC15437 hypothetical protein MGC15437
AF091092	p < 1e-07	CL683 weakly similar to glutathione peroxidase 2
AI609709	p < 1e-07	CXorf6 chromosome X open reading frame 6
BG236645	0.000003	ESTs
AF082868	p < 1e-07	BBOX1 butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1
BE326342	p < 1e-07	ESTs, highly similar to bK989H11.1 [H.sapiens]
AL080079	p < 1e-07	DKFZP564D0462 hypothetical protein DKFZP564D0462
AF181862	p < 1e-07	GPRC5B G protein-coupled receptor, family C, group 1, member B
		PRNP prion protein (p27-30) (Creutzfeldt-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)
BC012844	p < 1e-07	FOXD1 forkhead box D1
AA977269	p < 1e-07	

022041001010PC		
AA999973	p < 1e-07	FLJ14054 hypothetical protein FLJ14054
AW195038	p < 1e-07	KIP2 DNA-dependent protein kinase catalytic subunit-interacting protein 2
AA433906	p < 1e-07	KSP37 Ksp37 protein
AF070614	p < 1e-07	SCHIP1 schwannomin interacting protein 1
BF511352	p < 1e-07	LYN v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
BC011901	p < 1e-07	KRT17 keratin 17
N31940	p < 1e-07	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
BC002829	p < 1e-07	S100A2 S100 calcium binding protein A2
AL137332	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp434K2172 (from clone DKFZp434K2172)
AB022918	p < 1e-07	ST3GALVI alpha2,3-sialyltransferase
BC008709	p < 1e-07	ADD2 adducin 2 (beta)
AK026733	p < 1e-07	Homo sapiens cDNA: FLJ23080 fis, clone LNG06052
H10667	p < 1e-07	ROR1 receptor tyrosine kinase-like orphan receptor 1
X70340	p < 1e-07	TGFA transforming growth factor, alpha
Y15723	p < 1e-07	GUCY1A3 guanylate cyclase 1, soluble, alpha 3
NM_005044	p < 1e-07	PRKX protein kinase, X-linked
AB018329	p < 1e-07	KIAA0786 latrophilin
BF444945	p < 1e-07	HFRASLS HFRAS-like suppressor
BF589790	p < 1e-07	ADM adrenomedullin
AF132818	p < 1e-07	KLF5 Kruppel-like factor 5 (intestinal)
D11613	p < 1e-07	VSNL1 visinin-like 1
BC001275	p < 1e-07	ANXA1 annexin A1
M99487	p < 1e-07	FOLH1 folate hydrolase (prostate-specific membrane antigen) 1
AB052906	p < 1e-07	ULBP2 UL16 binding protein 2
BC012107	p < 1e-07	SH2D2A SH2 domain protein 2A
AA586749	0.0000001	KRT5 keratin 5 (epidermolysis bullosa simplex, Dowling-Meara/Kobner/Weber-Cockayne types)
BC017918	p < 1e-07	LOC64148 17kD fetal brain protein
NM_005378	p < 1e-07	MYCN v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)
AA767129	p < 1e-07	PRKY protein kinase, Y-linked
AW139720	p < 1e-07	FLJ12649 hypothetical protein FLJ12649
BC012432	p < 1e-07	FAT FAT tumor suppressor homolog 1 (Drosophila)
BC010003	p < 1e-07	Homo sapiens, clone IMAGE:4134852, mRNA, partial cds
AF155651	p < 1e-07	PAK3 p21 (CDKN1A)-activated kinase 3
BC018646	p < 1e-07	PLCG2 phospholipase C, gamma 2 (phosphatidylinositol-specific)

022041001010PC		
BC011705	p < 1e-07	COL9A3 collagen, type IX, alpha 3
AF242518	p < 1e-07	LOC57115 hypothetical protein SBI67
AL136755	p < 1e-07	DKFZP434A1315 hypothetical protein DKFZp434A1315
NM_001238	p < 1e-07	CCNE1 cyclin E1
AB023430	p < 1e-07	BIT brain-immunoglobulin-like molecule with tyrosine-based activation motifs
AL050374	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp586C1619 (from clone DKFZp586C1619)
AK056040	p < 1e-07	RE2 G-protein coupled receptor
BC007293	p < 1e-07	MGC15668 hypothetical protein MGC15668
AY004253	p < 1e-07	PRDM13 PR domain containing 13
BC012381	p < 1e-07	FLJ10430 hypothetical protein FLJ10430
AW118456	p < 1e-07	CRABP1 cellular retinoic acid binding protein 1
AF131789	p < 1e-07	DKFZP566A1524 hypothetical protein DKFZp566A1524
BC007382	p < 1e-07	MGC16212 hypothetical protein MGC16212
NM_014274	p < 1e-07	ABPZF Alu-binding protein with zinc finger domain
AF239820	p < 1e-07	C4ST chondroitin 4-sulfotransferase
AL389942	p < 1e-07	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2005635
AW574736	p < 1e-07	PRKCN protein kinase C, nu
AL136566	p < 1e-07	FLJ12783 hypothetical protein FLJ12783
BC012142	p < 1e-07	P5 protein disulfide isomerase-related protein
AI560801	p < 1e-07	PRSS12 protease, serine, 12 (neutrypsin, motopsin)
BC000765	p < 1e-07	MGC2742 hypothetical protein MGC2742
AK021728	p < 1e-07	Homo sapiens cDNA FLJ11666 fis, clone HEMBA1004672
AF051321	p < 1e-07	T-STAR Sam68-like phosphotyrosine protein, T-STAR
BE965331	p < 1e-07	CTSL2 cathepsin L2
R76294	p < 1e-07	ESTs
AL080235	p < 1e-07	RIS1 Ras-induced senescence 1
NM_002988	0.0000575	SCYA18 small inducible cytokine subfamily A (Cys-Cys), member 18, pulmonary and activation-regulated
BC009701	p < 1e-07	PD12 peptidyl arginine deiminase, type II
AF133059	p < 1e-07	NFE2L3 nuclear factor (erythroid-derived 2)-like 3
AF356193	p < 1e-07	CARD6 caspase recruitment domain family, member 6
BC009744	p < 1e-07	CSDA cold shock domain protein A
BC015663	p < 1e-07	TNRC3 trinucleotide repeat containing 3
BC010039	p < 1e-07	CLP coactosin-like protein
N47717	p < 1e-07	FABP5 fatty acid binding protein 5 (psoriasis-associated)

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AF280086	p < 1e-07	CHST6 carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6
AL117633	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp434E235 (from clone DKFZp434E235)
BC009010	p < 1e-07	Homo sapiens, clone MGC:18257 IMAGE:4158300, mRNA, complete cds
BC008568	p < 1e-07	CH13L1 chitinase 3-like 1 (cartilage glycoprotein-39)
BC005963	0.0000357	MAGEA3 melanoma antigen, family A, 3
BC010920	p < 1e-07	CLDN10 claudin 10
BC011460	p < 1e-07	CH13L2 chitinase 3-like 2
AF131235	p < 1e-07	CHST4 carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4
BC004411	p < 1e-07	HCA127 hepatocellular carcinoma-associated antigen 127
AK025347	p < 1e-07	KIAA1357 KIAA1357 protein
BC000563	p < 1e-07	SLC6A2 solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2
AF057352	p < 1e-07	IMP-2 IGF-II mRNA-binding protein 2
X77197	p < 1e-07	CLCN4 chloride channel 4
AF073515	p < 1e-07	CRLF1 cytokine receptor-like factor 1
AW172994	0.0000008	MMP12 matrix metalloproteinase 12 (macrophage elastase)
A1678454	p < 1e-07	MYO10 myosin X
AK025251	p < 1e-07	CHST3 carbohydrate (chondroitin 6) sulfotransferase 3
BC013300	p < 1e-07	STK12 serine/threonine kinase 12
BC010379	0.0000002	CSTA cystatin A (steffin A)
A1460151	0.0000025	ACTG2 actin, gamma 2, smooth muscle, enteric
BC013153	p < 1e-07	LOXL4 lysyl oxidase-like 4
BC007049	p < 1e-07	RGS2 regulator of G-protein signalling 2, 24kD
AK056666	p < 1e-07	Homo sapiens cDNA FLJ32104 fts, clone OCBBF2001307
BC000871	p < 1e-07	ANXA3 annexin A3
A1433792	p < 1e-07	ESTs
BC008952	p < 1e-07	LDHB lactate dehydrogenase B
AF083066	p < 1e-07	CHST2 carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2
NM_003878	p < 1e-07	G6H gamma-glutamyl hydrolase (conjugase, folypolyglutaminyl hydrolase)
AA631303	p < 1e-07	Homo sapiens prostate-specific membrane antigen PSM mRNA, exon 18 alternative splice variant, partial cds
AF336127	p < 1e-07	SLC4A11 solute carrier family 4, sodium bicarbonate transporter-like, member 11
AK026946	p < 1e-07	FLJ23293 likely ortholog of mouse ADP-ribosylation-like factor 6 interacting protein 2
BC015359	p < 1e-07	Homo sapiens, Similar to RIKEN cDNA 1810037C20 gene, clone MGC:21481 IMAGE:3852062, mRNA, complete cds
AJ420564	p < 1e-07	Homo sapiens cDNA: FLJ22314 fts, clone HRC05250

AF052126	p < 1e-07	SRD5A1 steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)
AK000708	p < 1e-07	FLJ20701 hypothetical protein FLJ20701
NM_003504	p < 1e-07	CDC45L CDC45 cell division cycle 45-like (S. cerevisiae)
BC000881	p < 1e-07	CENPA centromere protein A (17kD)
AI142639	p < 1e-07	ESTs
AK026790	p < 1e-07	Homo sapiens cDNA: FLJ23137 fis, clone LNG08842
AA761512	p < 1e-07	LPIN1 lipin 1
BC017293	p < 1e-07	MSN moesin
AL049977	0.000019	CLDN8 claudin 8
AL122077	p < 1e-07	DNAH17 dynein, axonemal, heavy polypeptide 17
BC003554	p < 1e-07	UBE2E3 ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)
AF245436	p < 1e-07	FLJ23518 hypothetical protein FLJ23518
AF333769	p < 1e-07	CASPR3 cell recognition molecule CASPR3
AB051513	p < 1e-07	KIAA1726 KIAA1726 protein
AA766903	p < 1e-07	ESTs, highly similar to A46297 beta-1,6-N-acetylglucosaminyltransferase [H.sapiens]
AI823561	p < 1e-07	LPL lipoprotein lipase
NM_002284	p < 1e-07	KRTHB6 keratin, hair, basic, 6 (monilethrix)
AA424146	p < 1e-07	LOC51312 mitochondrial solute carrier
AI200443	0.0000155	MAGEA5 melanoma antigen, family A, 5
H18932	p < 1e-07	XK Kell blood group precursor (McLeod phenotype)
BF062000	p < 1e-07	ESTs, highly similar to unnamed protein product [H.sapiens]
AF035594	p < 1e-07	Homo sapiens protein kinase C-alpha mRNA, partial 3' UTR
BC002895	p < 1e-07	GSTA2 glutathione S-transferase A2
AA648922	p < 1e-07	CDC25A cell division cycle 25A
BC004199	p < 1e-07	RLBP1 retinaldehyde binding protein 1
BC002947	p < 1e-07	FOLR1 folate receptor 1 (adult)
AA716439	p < 1e-07	BCE-1 BCE-1 protein
AI275604	p < 1e-07	PRRG1 proline-rich Gla (G-carboxyglutamic acid) polypeptide 1
BC017381	p < 1e-07	FLJ12929 hypothetical protein FLJ12929
AI188827	p < 1e-07	PIM1 pim-1 oncogene
AL080059	0.0000025	KIAA1750 KIAA1750 protein
AY037298	p < 1e-07	ELOVL4 elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4
AF245517	0.0000145	ATP6N1B ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1B
BC017730	p < 1e-07	TNFRSF21 tumor necrosis factor receptor superfamily, member 21

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BC018652	p < 1e-07	FXVD6 FXVD domain-containing ion transport regulator 6
A1741143	p < 1e-07	Homo sapiens cDNA FLJ32401 fis, clone SKMUS2000339
X64318	p < 1e-07	NFIL3 nuclear factor, interleukin 3 regulated
AB047783	p < 1e-07	ANKRD3 ankyrin repeat domain 3
AF038185	p < 1e-07	Homo sapiens clone 23700 mRNA sequence
BC016838	p < 1e-07	CPVL carboxypeptidase, vitellogenic-like
AF193809	p < 1e-07	RHCG Rh type C glycoprotein
AL420473	p < 1e-07	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1502032
AF285109	p < 1e-07	3-Sep sepin 3
NIM_001604	p < 1e-07	PAX6 paired box gene 6 (aniridia, keratitis)
BC009945	p < 1e-07	KIAA0746 KIAA0746 protein
AF026547	p < 1e-07	CSPG3 chondroitin sulfate proteoglycan 3 (neurocan)
AF101051	p < 1e-07	CLDN1 claudin 1
BC002710	p < 1e-07	KLK10 kallikrein 10
AA873846	p < 1e-07	LOC91689 hypothetical gene supported by AL449243
AL452634	p < 1e-07	GPR64 G protein-coupled receptor 64
AK027126	p < 1e-07	ASS argininosuccinate synthetase
AL420542	p < 1e-07	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1090104
AK024818	0.000002	MMP1 matrix metalloproteinase 1 (interstitial collagenase)
AW265278	p < 1e-07	INV invlucrin
AW445220	0.000015	HSJ001348 cDNA for differentially expressed CO16 gene
AF108138	p < 1e-07	PIF1 DNA helicase homolog PIF1
BC002660	p < 1e-07	TMOD tropomodulin
AA909006	p < 1e-07	LBP-32 LBP protein 32
AI097663	p < 1e-07	P450RAL-2 cytochrome P450 retinoid metabolizing protein
BC009742	p < 1e-07	LAD1 ladinin 1
AB028140	p < 1e-07	TMPRSS5 transmembrane protease, serine 5 (spinesin)
AI569989	p < 1e-07	KIAA1755 KIAA1755 protein
BF508352	p < 1e-07	DSG1 desmoglein 1
R49390	p < 1e-07	KIAA1678 KIAA1678
AI174254	p < 1e-07	Homo sapiens cDNA FLJ31586 fis, clone NT2RI200221
BE046069	p < 1e-07	ESTs
AL109775	p < 1e-07	SH3GL3 SH3-domain GRB2-like 3
AI522215	p < 1e-07	KIAA1804 KIAA1804 protein

BC008682	p < 1e-07	ARP3BETA actin-related protein 3-beta
L26584	p < 1e-07	RASGRF1 Ras protein-specific guanine nucleotide-releasing factor 1
AL136856	p < 1e-07	NTT5 NTT5 protein
AF038173	p < 1e-07	ATSV axonal transport of synaptic vesicles
NM_003360	p < 1e-07	UGT8 UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase)
BC015915	p < 1e-07	FZD7 frizzled homolog 7 (Drosophila)
BG939593	p < 1e-07	ANGPT1 angiopoietin 1
BF446789	p < 1e-07	CAV2 caveolin 2
AI538937	p < 1e-07	GDF5 growth differentiation factor 5 (cartilage-derived morphogenetic protein-1)
BC011672	p < 1e-07	KIAA0514 KIAA0514 gene product
AI494546	p < 1e-07	ICB-1 basement membrane-induced gene
BC008764	p < 1e-07	KNSL6 kinesin-like 6 (mitotic centromere-associated kinesin)
BC010358	p < 1e-07	CYP39A1 oxysterol 7alpha-hydroxylase
M14584	p < 1e-07	IL6 interleukin 6 (interferon, beta 2)
R41459	p < 1e-07	KIAA1136 KIAA1136 protein
AL157459	p < 1e-07	Homo sapiens mRNA, cDNA DKFZp434B0425 (from clone DKFZp434B0425)
BC001068	p < 1e-07	C20orf129 chromosome 20 open reading frame 129
AL133624	p < 1e-07	DKFZp434B1222 AKAP-binding sperm protein ropporin
AJ243500	p < 1e-07	TRPV6 transient receptor potential cation channel, subfamily V, member 6
AI950130	0.0000006	GZMB granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)
AK023678	p < 1e-07	Homo sapiens cDNA FLJ13616 fs, clone PLACE1010916
BC002325	0.0000019	MGC4309 hypothetical protein MGC4309
AB049586	p < 1e-07	B3GNT4 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4
AL136840	p < 1e-07	MCM10 MCM10 minichromosome maintenance deficient 10 (S. cerevisiae)
BC014039	p < 1e-07	KIAA0175 likely ortholog of maternal embryonic leucine zipper kinase
AL122086	p < 1e-07	TIAM2 T-cell lymphoma invasion and metastasis 2
AK055431	p < 1e-07	Homo sapiens cDNA FLJ30869 fs, clone FEBRA2004224
AW472810	p < 1e-07	IL12A interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)
BC010353	0.0000004	PTPLA protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a
BI493178	p < 1e-07	KIAA0161 KIAA0161 gene product
AA181334	p < 1e-07	TNNI2 tropoin I, skeletal, fast
AF067223	p < 1e-07	PDE9A phosphodiesterase 9A
BC010954	0.0000008	SCYB10 small inducible cytokine subfamily B (Cys-X-Cys), member 10
AI218529	p < 1e-07	KIAA1754 KIAA1754 protein

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AI380218	p < 1e-07	FLJ13385 hypothetical protein FLJ13385
BC013134	p < 1e-07	Homo sapiens, clone IMAGE:4512785, mRNA
AJ245600	p < 1e-07	Homo sapiens mRNA for hypothetical protein (TR2/D15 gene)
BC007609	p < 1e-07	Homo sapiens, Similar to hypothetical protein PRO1722, clone MGC:15692 IMAGE:3351479, mRNA, complete cds
AW589741	p < 1e-07	FLJ10159 hypothetical protein FLJ10159
BC016308	p < 1e-07	GRO3 GRO3 oncogene
BC013362	p < 1e-07	RUNX3 runt-related transcription factor 3
AI582813	p < 1e-07	CHRNA5 cholinergic receptor, nicotinic, alpha polypeptide 5
AI436812	p < 1e-07	ESTs, Weakly similar to hyperpolarization-activated cyclic nucleotide-gated channel hHCN2 [H.sapiens]
AF039843	p < 1e-07	SPRY2 sprouty homolog 2 (Drosophila)
AF097021	0.0003463	GW112 differentially expressed in hematopoietic lineages
AF054839	p < 1e-07	TSPAN-2 tetraspan 2
BC005029	p < 1e-07	FLJ10718 hypothetical protein FLJ10718
AL137580	p < 1e-07	C20orf130 chromosome 20 open reading frame 130
BF447279	0.0000004	ESTs
AI767898	0.0000015	GBP5 guanylate binding protein 5
AI140061	p < 1e-07	E2F3 E2F transcription factor 3
BI963794	p < 1e-07	PLA2G7 phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)
AI632467	p < 1e-07	OKB1 organic cation transporter OKB1
AI366784	p < 1e-07	TAF4B TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105 kD
AW204385	p < 1e-07	PDE7A phosphodiesterase 7A
AW451872	p < 1e-07	KIAA0173 KIAA0173 gene product
AL162059	p < 1e-07	TLE4 transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)
AA664218	p < 1e-07	ETV5 ets variant gene 5 (ets-related molecule)
AL136836	p < 1e-07	LOC51678 MAGUK protein p55T; Protein Associated with Lins 2
AL133590	p < 1e-07	WASF3 WAS protein family, member 3
AK058009	0.0000022	Homo sapiens cDNA FLJ25280 fis, clone STM06543
AI207256	p < 1e-07	Homo sapiens mRNA for FLJ00074 protein, partial cds
AL137281	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp434C2016 (from clone DKFZp434C2016)
BF433296	p < 1e-07	GBP1 guanylate binding protein 1, interferon-inducible, 67kD
AA714213	p < 1e-07	ESTs, Highly similar to T47163 hypothetical protein DKFZp762E1312.1 [H.sapiens]
BC013966	p < 1e-07	FLJ10156 hypothetical protein
AI082049	p < 1e-07	ESTs

U74612	p < 1e-07	FOXM1 forkhead box M1
W94858	p < 1e-07	GAS1 growth arrest-specific 1
B1492329	p < 1e-07	KIAA1214 KIAA1214 protein
AB041036	0.0001467	KLK11 kallikrein 11
AA931563	p < 1e-07	OR7E27P olfactory receptor, family 7, subfamily E, member 27 pseudogene
AF118070	p < 1e-07	DKFZp762A227 hypothetical protein DKFZp762A227
AI567843	p < 1e-07	ESTs, Weakly similar to JC5314 CDC28/cdc2-like kinase associating arginine-serine cyclophilin [H.sapiens]
BC006443	p < 1e-07	LRP8 low density lipoprotein receptor-related protein 8, apolipoprotein e receptor
AF178532	p < 1e-07	BACE2 beta-site APP-cleaving enzyme 2
AA205947	p < 1e-07	HHGP HHGP protein
U85267	p < 1e-07	DSCR1 Down syndrome critical region gene 1
AW290960	p < 1e-07	ESTs, Highly similar to T00391 hypothetical protein KIAA0612 [H.sapiens]
AK025747	p < 1e-07	FIGN fidgetin
AB027289	p < 1e-07	LOC51191 cyclin-E binding protein 1
L20470	p < 1e-07	VLDLR very low density lipoprotein receptor
BC015592	p < 1e-07	KIAA0937 KIAA0937 protein
AF247820	p < 1e-07	CALD1 caldesmon 1
AK000012	p < 1e-07	FLJ20005 hypothetical protein FLJ20005
AL157483	p < 1e-07	FLJ11264 hypothetical protein FLJ11264
AA810022	p < 1e-07	KIAA0846 KIAA0846 protein
AB048286	p < 1e-07	DGAT2 diacylglycerol O-acyltransferase homolog 2 (mouse)
BC017575	p < 1e-07	CHEK1 CHK1 checkpoint homolog (S. pombe)
AA877761	p < 1e-07	ESTs, Weakly similar to SYN1 MOUSE SYNAPSIN I [M.musculus]
AJ010277	p < 1e-07	TBX19 T-box 19
AF237763	0.0000112	GPR87 G protein-coupled receptor 87
AW874308	p < 1e-07	OR7E38P olfactory receptor, family 7, subfamily E, member 38 pseudogene
AF230904	p < 1e-07	SH3KBP1 SH3-domain kinase binding protein 1
Y16645	0.0000455	SCYA8 small inducible cytokine subfamily A (Cys-Cys), member 8 (monocyte chemotactic protein 2)
BC010466	p < 1e-07	B3GAT1 beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)
AK024298	p < 1e-07	Homo sapiens cDNA FLJ14236 fts, clone NT2RP400515
AK026095	p < 1e-07	SNTB1 syntrophin, beta 1 (dystrophin-associated protein A1, 59kD, basic component 1)
AK022914	p < 1e-07	Homo sapiens cDNA FLJ12852 fts, clone NT2RP2003445
AJ276230	p < 1e-07	PLD1 phospholipase D1, phosphatidylcholine-specific
AK022089	p < 1e-07	PAMC1 peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor

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AI023133	p < 1e-07	ESTs
BC002536	p < 1e-07	PFKP phosphofructokinase, platelet
NM_005401	p < 1e-07	PTPN14 protein tyrosine phosphatase, non-receptor type 14
AI350087	0.0000002	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PRECURSOR [H.sapiens]
NM_005409	0.0000011	SCYB11 small inducible cytokine subfamily B (Cys-X-Cys), member 11
AK024865	p < 1e-07	FLJ21212 hypothetical protein FLJ21212
BC015484	p < 1e-07	CALB2 calbindin 2, (29kD, calretinin)
AK025562	p < 1e-07	Homo sapiens cDNA: FLJ21909 fts, clone HEP03834
AI538226	0.0000006	GNG4 guanine nucleotide binding protein 4
AW409700	0.0000002	ESTs, Weakly similar to similar to ankyrin of Chromatium vinosum [H.sapiens]
AI656548	p < 1e-07	ESTs
AJ223366	0.0000019	Homo sapiens mRNA for OCIM (Oncogene in Multiple Myeloma) protein
AI524385	p < 1e-07	ANLN anillin, actin binding protein (scraps homolog, Drosophila)
AF241534	p < 1e-07	HYMAI hydatidiform mole associated and imprinted
BC004379	0.0000005	GJB5 gap junction protein, beta 5 (connexin 31.1)
BC012198	p < 1e-07	Homo sapiens, clone MGC:4408 IMAGE:2906200, mRNA, complete cds
AL136653	p < 1e-07	DEPP decidual protein induced by progesterone
AK026139	p < 1e-07	GJB3 gap junction protein, beta 3, 31kD (connexin 31)
BC012513	p < 1e-07	ARHE ras homolog gene family, member E
BC010044	p < 1e-07	CDC20 CDC20 cell division cycle 20 homolog (S. cerevisiae)
AL162079	p < 1e-07	SLC16A1 solute carrier family 16 (monocarboxylic acid transporters), member 1
BC000218	p < 1e-07	DL3 delta-like 3 (Drosophila)
AK000770	p < 1e-07	Homo sapiens cDNA FLJ20763 fts, clone COL09911
BC001211	p < 1e-07	KIFC3 kinesin family member C3
BC010612	p < 1e-07	Homo sapiens, clone IMAGE:4157546, mRNA, partial cds
BC003610	p < 1e-07	MFGEE8 milk fat globule-EGF factor 8 protein
AK025511	p < 1e-07	ATP11A ATPase, Class VI, type 11A
AF102848	0.0001895	HAIK1 type I intermediate filament cytokeratin
AL035878	0.0003777	DCX doublecortex, lissencephaly, X-linked (doublecortin)
AI188749	0.0000001	ESTs
AI004681	p < 1e-07	ESTs, Weakly similar to T33068 hypothetical protein C35E7.9 - Caenorhabditis elegans [C.elegans]
AA988024	0.0000093	FLJ14503 hypothetical protein FLJ14503
BC013106	p < 1e-07	RRAS2 related RAS viral (r-ras) oncogene homolog 2
BC006537	0.0001025	HOXA9 homeo box A9

BC007964	0.0000001	CD38 CD38 antigen (p45)
AA903532	0.0000001	SV2B synaptic vesicle protein 2B homolog
BC015839	p < 1e-07	Homo sapiens, clone IMAGE:4296901, mRNA
BC009232	0.0000005	Homo sapiens, Similar to G antigen 8, clone MGC:16513 IMAGE:3960352, mRNA, complete cds
AI015671	0.0000001	FLJ12604 hypothetical protein FLJ12604
D25538	p < 1e-07	ADCY7 adenylate cyclase 7
BC011000	p < 1e-07	MGC16386 similar to RIKEN cDNA 2610036L13
BM052808	p < 1e-07	KIAA0237 KIAA0237 gene product
AK026826	p < 1e-07	Homo sapiens cDNA: FLJ23173 fis, clone LNG10019
BC000078	0.0000001	MGC3279 hypothetical protein MGC3279 similar to collectins
AL049933	p < 1e-07	GNAI1 guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1
AF136631	p < 1e-07	LOC51299 neuritin
AW205836	p < 1e-07	RAB6B RAB6B, member RAS oncogene family
BC015640	0.0000005	CBR1 carbonyl reductase 1
AI654872	p < 1e-07	RASSF2 Ras association (RalGDS/AF-6) domain family 2
AF053305	p < 1e-07	BUB1 BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)
AF331521	p < 1e-07	SLC26A7 solute carrier family 26, member 7
AA993639	p < 1e-07	FLJ10748 hypothetical protein FLJ10748
AL157443	p < 1e-07	FAT2 FAT tumor suppressor homolog 2 (Drosophila)
BC007407	p < 1e-07	NMB neuromedin B
AL080058	p < 1e-07	DKFZP564G202 DKFZP564G202 protein
M59305	p < 1e-07	NPR3 natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)
BC000703	p < 1e-07	FLJ10468 hypothetical protein FLJ10468
S79869	p < 1e-07	HOXA1 homeo box A1
BC008584	0.0000021	BMP7 bone morphogenetic protein 7 (osteogenic protein 1)
BC008947	p < 1e-07	FLJ10540 hypothetical protein FLJ10540
BC008036	0.0000079	KLK5 kallikrein 5
BC012204	p < 1e-07	Homo sapiens, clone MGC:10002 IMAGE:3882800, mRNA, complete cds
BC001847	p < 1e-07	MGC4504 hypothetical protein MGC4504
AA088779	p < 1e-07	MFHAS1 malignant fibrous histiocytoma amplified sequence 1
AF177337	p < 1e-07	FLJ13391 hypothetical protein FLJ13391
AF283670	0.0000011	KLK14 kallikrein 14
BC015310	p < 1e-07	FLJ21069 hypothetical protein FLJ21069
AF201933	p < 1e-07	DC11 DC11 protein

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AL136820	p < 1e-07	KIAA1411 KIAA1411 protein
BC000260	p < 1e-07	AKR1E1 aldo-keo reductase family 1, member B1 (aldose reductase)
A1081342	p < 1e-07	OR7E37P olfactory receptor, family 7, subfamily E, member 37 pseudogene
BC007491	p < 1e-07	EXO1 exonuclease 1
AK026061	p < 1e-07	FLJ22408 hypothetical protein FLJ22408
W69074	p < 1e-07	S100A4 S100 calcium binding protein A4 (calcium protein, calyasculin, metastasin, murine placental homolog)
BC007707	0.000012	HEY2 hairy/enhancer-of-split related with YRPW motif 2
AK057943	0.000001	Homo sapiens cDNA FLJ25214 fls, clone REC08615
AF222980	p < 1e-07	DISC1 disrupted in schizophrenia 1
AF172852	p < 1e-07	CLSP calmodulin-like skin protein
A1569288	p < 1e-07	ESTs
AF153609	p < 1e-07	SGK serum/glucocorticoid regulated kinase
BF512938	p < 1e-07	RARB retinoic acid receptor, beta
A1633770	p < 1e-07	ESTs
BC014645	p < 1e-07	PRX2 paired determining region Y-box 9 (campomelic dysplasia, autosomal sex-reversal)
BC007951	0.000002	SOX9 SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal)
A1299541	p < 1e-07	ESTs
BC001940	p < 1e-07	DKFZp762E1312 hypothetical protein DKFZp762E1312
AA857853	0.000006	LCN2 lipocalin 2 (oncogene 24p3)
N22033	p < 1e-07	COL11A2 collagen, type XI, alpha 2
A1200706	0.000004	FLJ10134 hypothetical protein FLJ10134
BC010100	p < 1e-07	TLE1 transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)
BC010078	p < 1e-07	RISC likely homolog of rat and mouse retinoid-inducible serine carboxypeptidase
A1936089	0.000004	Homo sapiens cDNA FLJ14181 fls, clone NT2RP2004300
BC001207	0.000153	MAGE-E1 MAGE-E1 protein
AK056720	p < 1e-07	Homo sapiens cDNA FLJ32158 fls, clone PLACE600231
M86609	0.0000002	AKR1C1 aldo-keo reductase family 1, member C1 (dihydrodiol dehydrogenase 1, 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)
A1688729	p < 1e-07	ATP11C ATPase, Class VI, type 11C
J05428	0.000025	UGT2B7 UDP glycosyltransferase 2 family, polypeptide B7
A1298332	p < 1e-07	ESTs
A1097664	p < 1e-07	ESTs, Weakly similar to S23650 retrovirus-related hypothetical protein II [H.sapiens]
NM_002465	0.0000202	MYBPC1 myosin binding protein C, slow type
BF939405	p < 1e-07	EST

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AF166350	p < 1e-07	ST7 potential tumor suppressor
BC009401	p < 1e-07	NK4 natural killer cell transcript 4
BC009989	p < 1e-07	SMOH smoothened homolog (Drosophila)
AV655170	p < 1e-07	C21orf35 chromosome 21 open reading frame 35
BC005246	0.0001085	TM4SF3 transmembrane 4 superfamily member 3
AK024732	p < 1e-07	FLJ21079 hypothetical protein FLJ21079
NM_002281	p < 1e-07	KRTHB1 keratin, hair, basic, 1
ESTs, weakly similar to YK33_YEAST HYPOTHETICAL 46.5 KD PROTEIN IN MRS4-DYN1 INTERGENIC REGION [S.cerevisiae]		
AW293632	0.0000467	ODC1 ornithine decarboxylase 1
X55362	p < 1e-07	RGS20 regulator of G-protein signalling 20
AF060877	p < 1e-07	SAA1 serum amyloid A1
BC007022	0.0000109	SAA4 serum amyloid A4, constitutive
BC007026	p < 1e-07	Homo sapiens cDNA FLJ11980 fts, clone HEMBB1001304
AA643687	0.000722	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs
OR216 olfactory receptor, family 2, subfamily 1, member 6		
AI978664	p < 1e-07	PDL2 programmed death ligand 2
AW015394	0.0000083	Homo sapiens cDNA FLJ32375 fts, clone SALGL1000065, weakly similar to POLYHOMEOTIC-PROXIMAL
AW449368	p < 1e-07	CHROMATIN PROTEIN
ESTs		
AW139532	0.000027	SCYA5 small inducible cytokine A5 (RANTES)
AI278360	0.0000005	LBP-9 LBP protein; likely ortholog of mouse CRTTR-1
BF939156	0.0000005	ADAMDEC1 ADAM-like, decysin 1
AL137740	0.0001579	MGC2577 hypothetical protein MGC2577
AI924205	0.000124	CCKBR cholecystokinin B receptor
BC002551	p < 1e-07	FLJ14166 hypothetical protein FLJ14166
AF239668	p < 1e-07	NXPH4 neurexophilin 4
BC013353	0.0000001	HMG1Y high-mobility group (nonhistone chromosomal) protein isoforms I and Y
AW410306	0.0000021	CCNB2 cyclin B2
BC008832	p < 1e-07	ESTs
AL080146	p < 1e-07	
BE047139	p < 1e-07	
AL365412	0.0000115	LOC56932 hypothetical protein from EUROIMAGE 1759349

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BC008651	0.0002167	Homo sapiens, clone MGC:9913 IMAGE:3870821, mRNA, complete cds
AA398573	p < 1e-07	EIF5A2 eukaryotic translation initiation factor 5A2
AI457921	p < 1e-07	Homo sapiens cDNA FLJ11436 fis, clone HEMBA1001213
AF280546	p < 1e-07	NRP2 neuropilin 2
BF447302	p < 1e-07	ESTs
BC010091	p < 1e-07	BICD1 Bicaudal D homolog 1 (Drosophila)
AK026015	p < 1e-07	FLJ22352 hypothetical protein FLJ22362
BC014126	p < 1e-07	Homo sapiens, Similar to RIKEN cDNA 4932416D09 gene, clone IMAGE:4578228, mRNA, partial cds
U61374	p < 1e-07	SRPX sushi-repeat-containing protein, X chromosome
AI280215	0.0000014	ESTs
NM_001559	p < 1e-07	IL12RB2 interleukin 12 receptor, beta 2
BC011795	p < 1e-07	NDRG4 NDRG family member 4
AA903387	p < 1e-07	SIL TAL1 (SCL) interrupting locus
NM_021226	p < 1e-07	LOC58504 hypothetical protein from clones 23549 and 23762
BC009942	p < 1e-07	FLJ10628 hypothetical protein FLJ10628
AA772897	p < 1e-07	DNCH1 dynein, cytoplasmic, heavy polypeptide 1
BC006322	0.0000001	ATF3 activating transcription factor 3
AI765381	0.0000017	DJ434O14.3 hypothetical protein DJ434O14.3
BC007631	p < 1e-07	MGC15827 hypothetical protein MGC15827
AA937401	0.0006517	ESTs
BC001886	p < 1e-07	RRM2 ribonucleotide reductase M2 polypeptide
AK057339	0.0000005	LOC81569 actin like protein
BC007318	p < 1e-07	MAPRE2 microtubule-associated protein, RP/EB family, member 2
AA573096	p < 1e-07	FLJ10829 hypothetical protein FLJ10829
BC007656	p < 1e-07	UBE2C ubiquitin-conjugating enzyme E2C
BM055132	0.0000057	CFTR cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7)
AB011422	p < 1e-07	TRAD serine/threonine kinase with Dbl- and pleckstrin homology domains
BC016040	p < 1e-07	STK17B serine/threonine kinase 17b (apoptosis-inducing)
AK055323	p < 1e-07	Homo sapiens cDNA FLJ30761 fis, clone FEBRA2000538
BC005894	0.0000001	FMO2 flavin containing monooxygenase 2
NM_001078	0.0000011	VCAM1 vascular cell adhesion molecule 1
AL136819	p < 1e-07	DKFZP434G2226 hypothetical protein DKFZp434G2226
AF054993	0.0000008	SNAP91 synaptosomal-associated protein, 91 kD homolog (mouse)
AY044429	p < 1e-07	IL22RA2 class II cytokine receptor

AB033109	0.0000196	KIAA1283 KIAA1283 protein
AI871458	p < 1e-07	ESTs
AI569068	0.0000063	ESTs
AK056817	p < 1e-07	Homo sapiens cDNA FLJ32255 fis, clone PROST1000226
BC006267	0.0000711	FLJ22316 hypothetical protein FLJ22316
AA810180	p < 1e-07	FLJ10517 hypothetical protein FLJ10517
AF017790	p < 1e-07	HEC highly expressed in cancer, rich in leucine heptad repeats
BC010935	0.0000241	CSN10 casein, kappa
AI741771	p < 1e-07	RYR3 ryanodine receptor 3
		Homo sapiens cDNA FLJ30553 fis, clone BRAWH2003689, highly similar to Mus musculus clone mouse1-9
H06285	p < 1e-07	putative protein phosphatase type 2C mRNA
AA613572	p < 1e-07	ESTs
AL512731	0.0000001	Homo sapiens mRNA: cDNA DKFZp667B0711 (from clone DKFZp667B0711)
W57704	0.0000001	CNGA1 cyclic nucleotide gated channel alpha 1
BF224101	p < 1e-07	DOCK3 dedicator of cyto-kinesis 3
AJ420539	p < 1e-07	DEK DEK oncogene (DNA binding)
D10522	p < 1e-07	MARCKS myristoylated alanine-rich protein kinase C substrate
BC008691	p < 1e-07	RSU1 Ras suppressor protein 1
AF207664	p < 1e-07	ADAMTS1 a disintegrin-like and metalloprotease (repolysin type) with thrombospondin type 1 motif, 1
AF070592	p < 1e-07	HSKM-B HSKM-B protein
AK025290	p < 1e-07	ATP10B ATPase, Class V, type 10B
BC001749	p < 1e-07	WNT5B wingless-type MMTV integration site family, member 5B
AK025425	p < 1e-07	MGC21854 hypothetical protein MGC21854
AA642589	p < 1e-07	SEMG2 semenogelin II
BC010116	0.0000001	Homo sapiens, clone MGC:19762 IMAGE:3636045, mRNA, complete cds
NM_002510	0.0000001	GNPMB glycoprotein (transmembrane) nmbl
BC002744	p < 1e-07	MGC4090 hypothetical protein MGC4090
AA574056	p < 1e-07	OR7E119P olfactory receptor, family 7, subfamily A, member 119 pseudogene
AI500430	0.0000052	KIAA1909 KIAA1909 protein
AI972591	0.0000062	ESTs
AA232651	p < 1e-07	SUV39H2 suppressor of variegation 3-9 (Drosophila) homolog 2; hypothetical protein FLJ23414
BC009238	p < 1e-07	TUBA1 tubulin, alpha 1 (testis specific)
NM_022977	p < 1e-07	FACL4 fatty-acid-Coenzyme A ligase, long-chain 4
BC001844	0.0000001	MEIS2 Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse)

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N51717	0.0000117	ESTs
BC010658	p < 1e-07	KIAA0008 KIAA0008 gene product
BC013200	0.0000001	LCK lymphocyte-specific protein tyrosine kinase
AF027866	p < 1e-07	SERPINEB serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 7
AK026964	p < 1e-07	FLJ23311 hypothetical protein FLJ23311
BC010923	0.0000002	CART1 cartilage paired-class homeoprotein 1
R38438	p < 1e-07	SLC15A2 solute carrier family 15 (H+/peptide transporter), member 2
AL110202	p < 1e-07	PORININ pro-oncosis receptor inducing membrane injury gene
AK025215	0.0000001	FLJ21562 hypothetical protein FLJ21562
D90239	0.0005882	GLDC glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system protein P)
Al636660	p < 1e-07	C21orf31 chromosome 21 open reading frame 91
BC000633	p < 1e-07	TTK TTK protein kinase
BF511873	p < 1e-07	ESTs
Al816719	0.0000012	KIAA1870 KIAA1870 protein
AF053306	p < 1e-07	BUB1B BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)
NM_005257	0.0000001	GATA6 GATA binding protein 6
BC011920	p < 1e-07	FLJ20896 hypothetical protein FLJ20896
X12892	0.000001	PROS1 protein S (alpha)
M62925	p < 1e-07	TGM1 transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase)
AF239821	0.0000003	GALNAC4ST-2 GalNAc-4-sulfotransferase 2
BF437448	p < 1e-07	EST
AF098482	p < 1e-07	PSIP1 PC4 and SFRS1 interacting protein 1
Al096342	p < 1e-07	RGCC32 RGCC32 protein
BC015706	p < 1e-07	Homo sapiens, Similar to FLKEN cDNA 2810433K01 gene, clone MGC:10200 IMAGE:3909951, mRNA, complete cds
BC011561	0.0000001	HEPH hephaestin
AA903183	0.0000011	IL2RA interleukin 2 receptor, alpha
NM_001237	p < 1e-07	CCNA2 cyclin A2
AL137502	p < 1e-07	RAGD Rag D protein
BC006359	p < 1e-07	INA internexin neuronal intermediate filament protein, alpha
BF592799	p < 1e-07	PRKCO protein kinase C, theta
Al697249	0.0000294	EBI2 Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)
BC016719	0.000725	Homo sapiens, clone IMAGE:4070464, mRNA, partial cds
AF014398	p < 1e-07	IMPA2 inositol(myo)-1(or 4)-monophosphatase 2

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AL136828	0.0000001	DKFZP434K0427 hypothetical protein DKFZp434K0427
AI972473	0.0000723	EST
AW104435	0.0000002	UBE2E2 ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)
MT4447	p < 1e-07	TAP2 transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)
NM_005048	0.000801	PTHr2 parathyroid hormone receptor 2
AK024854	p < 1e-07	DJ742C19.2 phorbollin (similar to apolipoprotein B mRNA editing protein)
AK027274	p < 1e-07	Homo sapiens cDNA FLJ14368 fis, clone HEMBA1001122
AF147204	0.0000002	CXCR4 chemokine (C-X-C motif), receptor 4 (fusin)
BC005232	p < 1e-07	RPP38 ribonuclease P (38kD)
BC004897	0.0000011	CA3 carbonic anhydrase III, muscle specific
NM_002963	0.0000573	S100A7 S100 calcium binding protein A7 (psoriasin 1)
AF154845	0.0000003	MARK1 MAP/microtubule affinity-regulating kinase 1
AK000659	p < 1e-07	MT-ACT48 Mitochondrial Acyl-CoA Thioesterase
AJ420567	p < 1e-07	AMD1 S-adenosylmethionine decarboxylase 1
AF030942	p < 1e-07	PPP1R14BP1 protein phosphatase 1, regulatory (inhibitor) subunit 14B pseudogene 1
AL359561	p < 1e-07	DKFZP762N2316 hypothetical protein DKFZp762N2316
NM_002417	p < 1e-07	MKI67 antigen identified by monoclonal antibody Ki-67
NM_003503	p < 1e-07	CDC7L1 CDC7 cell division cycle 7-like 1 (S. cerevisiae)
AA084672	0.0000034	MSI1 musashi homolog 1 (Drosophila)
AL136919	p < 1e-07	DKFZp586J1119 hypothetical protein DKFZp586J1119
BC001051	p < 1e-07	ARL7 ADP-ribosylation factor-like 7
AF136715	0.0000176	TRAG3 taxol resistance associated gene 3
X97868	0.0000001	ARSF arylsulfatase F
AI568024	0.0000032	LAMB3 laminin, beta 3 (nicein (125kD), kalinin (140kD), BM600 (125kD))
AW191026	0.0000001	PLSCR1 phospholipid scramblase 1
BC017705	p < 1e-07	KNSL5 kinesin-like 5 (mitotic kinesin-like protein 1)
AB032698	0.0000007	BIN2 bridging integrator 2
BC001692	0.0000005	SLC2A5 solute carrier family 2 (facilitated glucose/fructose transporter), member 5
AB043585	0.0000001	REPRIMO candidate mediator of the p53-dependent G2 arrest
AA262504	p < 1e-07	EYA3 eyes absent homolog 3 (Drosophila)
BC017656	p < 1e-07	MONDOA Mix interactor
AK055596	p < 1e-07	Homo sapiens cDNA FLJ31034 fis, clone HSYRA1000178
NM_000057	p < 1e-07	BLM Bloom syndrome
BC012527	0.0000001	HIF1A hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)

022041001010PC		
BF196234	0.0000026	ESTs
AA805970	0.0000034	KIAA0275 KIAA0275 gene product
AL050066	p < 1e-07	NTT73 homolog of rat orphan transporter v7-3
AF339763	p < 1e-07	ABCC4 ATP-binding cassette, sub-family C (CFTR/MRP), member 4
AW189851	0.0000008	CUGBP2 CUG triplet repeat, RNA binding protein 2
NM_003122	0.0000169	SPINK1 serine protease inhibitor, Kazal type 1
AA826489	0.0000001	MY040 hypothetical brain protein my040
AK000054	p < 1e-07	FLJ20047 hypothetical protein FLJ20047
AI653207	p < 1e-07	ESTs
AL137735	p < 1e-07	ASB2 ankyrin repeat and SOCS box-containing 2
AI273114	p < 1e-07	ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]
BI492625	p < 1e-07	Homo sapiens cDNA FLJ30075 fis, clone BGG111000285
NM_006235	0.0002076	POU2AF1 POU domain, class 2, associating factor 1
AK000208	p < 1e-07	Homo sapiens cDNA FLJ20201 fis, clone COLF1210
AI669751	0.0000664	ZIP2 zinc transporter
BF513300	p < 1e-07	KIAA0074 KIAA0074 protein
M15990	p < 1e-07	YES1 v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1
BE671269	p < 1e-07	HAAO 3-hydroxyanthranilate 3,4-dioxygenase
BC000404	p < 1e-07	TRIP13 thyroid hormone receptor interactor 13
AL050388	0.0000001	Homo sapiens mRNA; cDNA DKFZp564M2422 (from clone DKFZp564M2422); partial cds
BC014526	0.0000024	ANKH ankylosis, progressive homolog (mouse)
BC007585	p < 1e-07	MYBL2 v-myb myeloblastosis viral oncogene homolog (avian)-like 2
AK025926	0.0000002	AK3 adenylate kinase 3
BC005127	p < 1e-07	ADFP adipose differentiation-related protein
AK054683	p < 1e-07	Homo sapiens cDNA FLJ30121 fis, clone BRACE1000084
BE206076	p < 1e-07	ALK anaplastic lymphoma kinase (Ki-1)
R05446	p < 1e-07	KIAA1424 KIAA1424 protein
BC003684	0.0000076	CXADR coxsackie virus and adenovirus receptor
BC016451	p < 1e-07	ADAMTS3 a disintegrin-like and metalloprotease (repolysin type) with thrombospondin type 1 motif, 3
AF070609	p < 1e-07	SLC1A3 solute carrier family 1 (glial high affinity glutamate transporter), member 3
BF724533	p < 1e-07	MGC3169 hypothetical protein MGC3169
AB053172	p < 1e-07	CDT1 DNA replication factor
AF124735	0.0005833	LHX2 LIM homeobox protein 2
AL157471	0.0000189	KIAA1500 KIAA1500 protein

AF326731	p < 1e-07	NUF2R hypothetical protein NUF2R
BC013767	p < 1e-07	Homo sapiens, Similar to RIKEN cDNA 2610528G05 gene, clone IMAGE:3875837, mRNA, partial cds
AA827777	p < 1e-07	ESTs
NM_006329	p < 1e-07	FBLN5 fibulin 5
BC014018	p < 1e-07	FLJ11196 hypothetical protein FLJ11196
BE047394	0.0000013	ESTs, Weakly similar to S71512 hypothetical protein T2 - mouse [M.musculus]
AW079735	0.0000016	SPRR2B small proline-rich protein 2B
AK023080	p < 1e-07	HSNOV1 novel protein
AL134596	0.0002539	ATP2B2 ATPase, Ca++ transporting, plasma membrane 2
AF331796	p < 1e-07	HCAP-G chromosome condensation protein G
AF329840	p < 1e-07	ZSIG37 G protein coupled receptor interacting protein, complement-c1q tumor necrosis factor-related
R40565	p < 1e-07	FYN FYN oncogene related to SRC, FGR, YES
BC002700	0.0000032	KRT7 keratin 7
AA877996	0.0002536	ESTs, Weakly similar to J05314 CDC28/cdc2-like kinase associating arginine-serine cyclophilin [H.sapiens]
R48461	0.0000037	ESTs
AA730123	0.0000001	PRDM1 PR domain containing 1, with ZNF domain
AF230495	0.00002	DUOX1 dual oxidase 1
AL039118	0.0000661	FOXG1B forkhead box G1B
AF146761	0.0001401	BLAME BCM-like membrane protein precursor
BC012885	0.0000035	TEM7R tumor endothelial marker 7-related precursor
AK026949	0.0000964	ZNF300 kruppel-like zinc finger protein
AF130988	p < 1e-07	EDAR ectodysplasin 1, anhidrotic receptor
AA489383	p < 1e-07	BMP2 bone morphogenetic protein 2
AF245356	p < 1e-07	TES testis derived transcript (3 LIM domains)
		ESTs, Weakly similar to FATH_HUMAN CADHERIN-RELATED TUMOR SUPPRESSOR HOMOLOG
AI184027	0.0000001	PRECURSOR [H.sapiens]
AI687303	0.0000032	GPR49 G protein-coupled receptor 49
BC000715	0.0000108	CLECSF9 C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 9
H05918	0.0000019	KIAA1867 KIAA1867 protein
BF437096	0.0000015	EST
AI193122	0.0000124	CYYR1 cysteine and tyrosine-rich 1
AK027009	0.0002318	FLJ23356 hypothetical protein FLJ23356
AI274576	p < 1e-07	CTSC cathepsin C
M90366	0.000042	ZP2 zona pellucida glycoprotein 2 (sperm receptor)

022041001010PC		
AY026763	p < 1e-07	GOA gene overexpressed in astrocytoma
AI049877	p < 1e-07	KIAA0186 KIAA0186 gene product
R85380	p < 1e-07	ESTs
AA812178	0.0000001	TLR1 toll-like receptor 1
U18548	p < 1e-07	GPR12 G protein-coupled receptor 12
AK000381	p < 1e-07	FLJ20374 hypothetical protein FLJ20374
BC001346	0.0000005	LOC51700 cytochrome b5 reductase b5R.2
U87460	0.0000026	GPR37 G protein-coupled receptor 37 (endothelin receptor type B-like)
AW137459	0.0000029	TMOD2 tropomodulin 2 (neuronal)
AA485276	0.0005783	CRTAC1 cartilage acidic protein 1
AI283489	0.0000008	FACL2 fatty-acid-Coenzyme A ligase, long-chain 2
AI433440	p < 1e-07	TNFAIP3 tumor necrosis factor, alpha-induced protein 3
BC010940	p < 1e-07	AIM2 absent in melanoma 2
AF202636	0.0000004	ANGPTL4 angiopoietin-like 4
BC012126	0.0000002	CLDN14 claudin 14
BC000748	0.0000003	TUBB4 tubulin, beta, 4
AK025320	p < 1e-07	SCEL scellin
NM_003662	0.0000016	PIR Pirin
AL133105	0.0000055	DKFZp434F2322 hypothetical protein DKFZp434F2322
AK001643	0.000527	FLJ10781 hypothetical protein FLJ10781
AW511572	0.0000029	FZD6 frizzled homolog 6 (Drosophila)
AI796505	p < 1e-07	HOXA2 homeo box A2
BF513683	p < 1e-07	GAJ GAJ protein
BC008283	0.0000169	CCK cholecystokinin
NM_001784	p < 1e-07	CD97 CD97 antigen
BC007633	p < 1e-07	EIF2C2 eukaryotic translation initiation factor 2C, 2
BC011403	p < 1e-07	GABRA5 gamma-aminobutyric acid (GABA) A receptor, alpha 5
BC002812	p < 1e-07	CBR3 carbonyl reductase 3
BC003630	0.0000048	KRT4 keratin 4
AI362949	0.0000242	ESTs
AW138010	0.0001317	SAA2 serum amyloid A2
NM_005985	p < 1e-07	SNAIL snail 1 homolog, zinc finger protein (Drosophila)
BC012609	p < 1e-07	SERPINE2 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2
BC010128	0.0000005	FLJ10970 hypothetical protein FLJ10970

022041001010PC		
AK025309	0.0000032	C1S complement component 1, s subcomponent
NM_025245	0.0000001	PBX4 pre-B-cell leukemia transcription factor 4
BF507686	p < 1e-07	CERD4 cer-d4 (mouse) homolog
AA731869	0.0002721	CD1A CD1A antigen, a polypeptide
AK000193	p < 1e-07	FLJ20186 hypothetical protein FLJ20186
BC015859	p < 1e-07	Homo sapiens, clone MGC:27381 IMAGE:4689539, mRNA, complete cds
AL136855	p < 1e-07	DKFZp434K2435 hypothetical protein DKFZp434K2435
AF089868	p < 1e-07	MCAM melanoma cell adhesion molecule
AL360258	0.0000009	FLJ11175 hypothetical protein FLJ11175
AK026248	p < 1e-07	FLJ22595 hypothetical protein FLJ22595
AI669793	p < 1e-07	ESTs
BC017840	0.0003003	Homo sapiens, clone IMAGE:4689305, mRNA, partial cds
BF112017	p < 1e-07	KCNE1L potassium voltage-gated channel, Isk-related family, member 1-like
AI375142	0.0000095	LOC57822 hypothetical protein LOC57822
BC002377	p < 1e-07	PTK7 PTK7 protein tyrosine kinase 7
AB040057	0.0000006	MST4 serine/threonine protein kinase MASK
AF027299	p < 1e-07	EPB41L2 erythrocyte membrane protein band 4.1-like 2
AK026659	0.0000003	Homo sapiens cDNA: FLJ23006 fts, clone LNC00414
AF078749	0.0000014	SLC22A3 solute carrier family 22 (extraneuronal monoamine transporter), member 3
AF277375	p < 1e-07	KIF4A kinesin family member 4A
AA747541	0.0000033	MYBL1 v-myb myeloblastosis viral oncogene homolog (avian)-like 1
BC007921	0.0000042	SPIB Spi-B transcription factor (Spi-1/PU.1 related)
AI823489	0.0005112	BARX2 BarH-like homeobox 2
NM_004233	p < 1e-07	CD83 CD83 antigen (activated B lymphocytes, immunoglobulin superfamily)
AI886575	p < 1e-07	ESTs
AI439152	0.0000001	KIAA1145 KIAA1145 protein
NM_019035	0.0000022	PCDH18 protocadherin 18
BF109847	0.0000025	ESTs
AL137558	0.0000353	VANGL2 vang, van gogh-like 2 (Drosophila)
AI553863	p < 1e-07	KIAA1204 KIAA1204 protein
AA866043	p < 1e-07	CBS cystathionine-beta-synthase
AW341053	p < 1e-07	ESTs
AK025912	0.0000004	COL4A2 collagen, type IV, alpha 2
AA634391	p < 1e-07	MAGEB4 melanoma antigen, family B, 4

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AI475447	0.0000043	FLJ12567 hypothetical protein FLJ12567
NM_005430	p < 1e-07	WNT1 wingless-type MMTV integration site family, member 1
NM_001998	p < 1e-07	FBLN2 fibulin 2
AI803166	0.0000007	ESTs
AL040372	p < 1e-07	ESTs, Weakly similar to A54854 Ras GTPase activating protein-related protein [H.sapiens]
BC012385	p < 1e-07	FBG4 F-box protein FBG4
AF045888	0.0000001	DNMT2 DNA (cytosine-5-)-methyltransferase 2
AA588167	0.0000004	KIAA1729 KIAA1729 protein
AF051152	0.0000006	TLR2 toll-like receptor 2
AL136550	0.0000077	BCMP1 brain cell membrane protein 1
AI969883	p < 1e-07	EST
AK026181	0.000001	Homo sapiens cDNA: FLJ22528 fis, clone HRC12825
AI469557	0.0000026	EPHB3 EphB3
AB037670	0.0000007	SLC7A10 solute carrier family 7, (cationic amino acid transporter, y ⁺ system) member 10
AK027157	p < 1e-07	DKFZp547N157 hypothetical protein DKFZp547N157
AB000520	p < 1e-07	APS adaptor protein with pleckstrin homology and src homology 2 domains
AW204447	0.0000005	OATP4P4 organic anion transporter polypeptide-related protein 4
AI420520	0.0000813	MGC12335 hypothetical protein MGC12335
AF146796	p < 1e-07	SLC34A2 solute carrier family 34 (sodium phosphate), member 2
BC010659	0.0008625	FLJ12691 hypothetical protein FLJ12691
AA732224	p < 1e-07	ESTs
AL136889	p < 1e-07	DKFZp434B227 hypothetical protein DKFZp434B227
AW193227	p < 1e-07	ESTs
AK024680	0.0000032	PRO2714 hypothetical protein PRO2714
AW069753	0.000012	CTGF connective tissue growth factor
NM_004532	0.0000654	MUC4 mucin 4, tracheobronchial
AF008203	0.0000116	ALX3 aristaless-like homeobox 3
BF513361	p < 1e-07	MAP2 microtubule-associated protein 2
BF507741	p < 1e-07	AF15Q14 AF15q14 protein
BC011587	0.0000108	Homo sapiens, Similar to RIKEN cDNA 1700018O18 gene, clone IMAGE:4121436, mRNA, partial cds
NM_002514	0.0000778	NOV nephroblastoma overexpressed gene
AA573170	0.0000001	EST
AK000520	0.0002189	FLJ20513 hypothetical protein FLJ20513
AI459117	p < 1e-07	C6orf34 chromosome 6 open reading frame 34

AF011468	p < 1e-07	STK15 serine/threonine kinase 15
AI269345	0.0001152	FLJ10851 hypothetical protein FLJ10851
AL050151	p < 1e-07	Homo sapiens mRNA, cDNA DKFZp586J0720 (from clone DKFZp586J0720)
AI042183	0.0000001	TP53BP2 tumor protein p53 binding protein, 2
AI307682	0.000746	IL18RAP interleukin 18 receptor accessory protein
AL136712	0.0000795	KIAA0820 KIAA0820 protein
BC000209	p < 1e-07	MGC2603 hypothetical protein MGC2603
AK026777	0.0000001	KIAA1573 KIAA1573 protein
AJ002367	p < 1e-07	SHOX2 short stature homeobox 2
AK025624	0.0000144	MGC5350 hypothetical protein MGC5350
BC016047	0.0000063	Homo sapiens, Similar to RIKEN cDNA 2310014B08 gene, clone IMAGE:4639904, mRNA, partial cds
BC010904	p < 1e-07	FLJ11252 hypothetical protein FLJ11252
NM_004609	0.0000003	TCF15 transcription factor 15 (basic helix-loop-helix)
BC002654	p < 1e-07	TUBB-5 tubulin beta-5
NM_052813	0.0000001	CARD9 caspase recruitment domain family, member 9
AA864938	0.0000005	LALBA lactalbumin, alpha-
BC012136	0.0000022	FLJ10160 hypothetical protein FLJ10160 similar to insulin related protein 2
BC001969	0.0000153	ROBO1 roundabout, axon guidance receptor, homolog 1 (Drosophila)
AL137736	p < 1e-07	Homo sapiens mRNA, cDNA DKFZp586P2321 (from clone DKFZp586P2321)
U64197	0.0000001	SCYA20 small inducible cytokine subfamily A (Cys-Cys), member 20
BE465918	0.0000005	VNN1 vanin 1
X78202	0.0001038	FOXG1A forkhead box G1A
AF329454	0.0004222	TMPPRSS2 transmembrane protease, serine 2
BC011268	0.0000001	KIAA1796 KIAA1796 protein
BC013919	0.0000001	TYMS thymidylate synthetase
AB058769	0.0003505	KIAA1866 KIAA1866 protein
BC005300	0.0004476	DTNA dystrobrevin, alpha
AI199268	0.0000006	Homo sapiens, Similar to RIKEN cDNA 2010317E24 gene, clone IMAGE:3502019, mRNA, partial cds
X53587	0.0000001	ITGB4 integrin, beta 4
BF111883	0.0000093	ba430M15.1 novel protein (ortholog of rat four repeat ion channel)
AF035279	0.0000001	IL15RA interleukin 15 receptor, alpha
NM_004936	0.0000147	CDKN2B cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
AK000364	0.0000001	KIAA1416 KIAA1416 protein
AF281255	0.0000014	BCLG apoptosis regulator BCL-G

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AK026265	0.0000121	FLJ22512 hypothetical protein FLJ22612
AA515100	0.0001378	ESTs
AA461301	0.000014	Homo sapiens nanos mRNA, partial cds
AF007133	0.000076	SIAT1 sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase)
AF186780	0.0000009	RGL RalGDS-like gene
		Homo sapiens cDNA: FLJ22401 fis, clone HRC08032, highly similar to AB027466 Homo sapiens SPON2 mRNA for spordin 2
AK026054	0.0000025	PSCD3 pleckstrin homology, Sec7 and coiled/coiled domains 3
BC008191	p < 1e-07	SPON2 spordin 2, extracellular matrix protein
BC002707	0.0000011	TM4SF4 transmembrane 4 superfamily member 4
BC001386	0.0000015	RCN1 reticulocalbin 1, EF-hand calcium binding domain
BC010120	p < 1e-07	CDH2 cadherin 2, type 1, N-cadherin (neuronal)
NM_001792	0.000069	ATP11B ATPase, Class VI, type 11B
AL133061	0.0000001	TSA1902 eosinophil chemotactic cytokine
AF290004	p < 1e-07	HS3ST1 heparan sulfate (glucosamine) 3-O-sulfotransferase 1
AF019386	0.0000011	Homo sapiens, clone IMAGE:4332938, mRNA
BC017409	0.0002052	STAG3 stromal antigen 3
AA747738	0.0000004	FLJ20330 hypothetical protein
AK000337	0.0000003	EBAF endometrial bleeding associated factor (left-right determination, factor A, transforming growth factor beta superfamily)
AF081513	p < 1e-07	Homo sapiens clone 25218 mRNA sequence
AF131762	0.0000001	DPYSL2 dihydropyrimidinase-like 2
U97105	0.0000002	DKFZp761C07121 hypothetical protein DKFZp761C07121
AL137308	0.000041	CRMP5 collapsin response mediator protein-5; CRMP3-associated molecule
AW139156	0.0000001	HOXA4 homeo box A4
M74297	p < 1e-07	Homo sapiens cDNA FLJ30824 fis, clone FEBRA2001698
AK055386	0.0000751	Homo sapiens mRNA; cDNA DKFZp434F152 (from clone DKFZp434F152)
AL096737	p < 1e-07	DUOX2 dual oxidase 2
AF267981	0.0000001	FLJ21162 hypothetical protein FLJ21162
AF277289	0.0000005	SATB1 special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's)
BG655508	0.000001	LOC57228 hypothetical protein from clone 643
BC001400	p < 1e-07	ESTs
BF195312	0.000023	PAM peptidylglycine alpha-amidating monooxygenase
BC018127	0.0000141	C21orf37 chromosome 21 open reading frame 37
N56968	p < 1e-07	

AI203899	0.000001	EPIM epimorphin
BC000117	p < 1e-07	GMD5 GDP-mannose 4,6-dehydratase
AJ276678	0.000001	C20orf32 chromosome 20 open reading frame 32
AK056230	0.000105	Homo sapiens cDNA FLJ31668 fis, clone NT2RI2004916
AL137461	p < 1e-07	Homo sapiens mRNA; cDNA DKFZp434K0621 (from clone DKFZp434K0621); partial cds
AF140242	0.0000048	OPN3 opsin 3 (encephalopsin, panopsin)
AF161508	p < 1e-07	HSPC159 HSPC159 protein
AJ251830	0.0000059	PIGPC1 p53-induced protein PIGPC1
BC002641	0.0000064	KRT15 keratin 15
AF161505	0.000013	HSPC156 HSPC156 protein
AA923424	0.0001192	ESTs, Weakly similar to I54374 gene NF2 protein [H.sapiens]
AL157432	p < 1e-07	TERA TERA protein
AK025494	0.0000003	FLJ21841 hypothetical protein FLJ21841
AK022869	0.0000001	Homo sapiens cDNA FLJ12807 fis, clone NT2RP2002316
BC008765	p < 1e-07	SDC1 syndecan 1
AI383975	0.0000034	SPRR2A small proline-rich protein 2A
BE328136	0.0000034	DPYSL3 dilydroxyrimidinase-like 3
AF106912	0.0000003	WSX1 class I cytokine receptor
BG054505	p < 1e-07	ESTs
BC008442	p < 1e-07	TM4SF1 transmembrane 4 superfamily member 1
BE045473	p < 1e-07	EST
R41498	0.0000002	KIAA0231 KIAA0231 protein
BC004277	p < 1e-07	FLJ10719 hypothetical protein FLJ10719
BF509349	p < 1e-07	Homo sapiens cDNA: FLJ23020 fis, clone LNG00943
AA910884	0.0000202	ESTs
AA810953	0.0000001	BIC Homo sapiens BIC noncoding mRNA, complete sequence
M84757	0.0000668	SPRR1B small proline-rich protein 1B (cornifin)
AL359605	0.0000752	Homo sapiens mRNA; cDNA DKFZp547G036 (from clone DKFZp547G036)
L40377	0.0000001	SERPINB8 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 8
AL136932	0.0000001	KIAA0922 KIAA0922 protein
BE348529	0.0001864	ESTs, Weakly similar to :SYN1 MOUSE SYNAPSIN I [M.musculus]
AI269387	0.0000001	BAG2 BCL2-associated athanogene 2
BF434466	0.0000572	ITGAB integrin, alpha 6
AI251449	0.0000037	ESTs

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AF063020	0.0000071	PSIP2 PC4 and SFRS1 interacting protein 2
AF285592	p < 1e-07	FTHL17 ferritin, heavy polypeptide-like 17
AL110124	0.0000017	DKFZP564A24.16 DKFZP564A24.16 protein
AA521246	0.0000054	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
AA844695	0.0000014	ESTs
AI566899	0.0000195	NFIX nuclear factor I/X (C/CAAT-binding transcription factor)
BF512918	0.0001109	AGC1 aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan, antigen identified by monoclonal antibody A0122)
L20971	0.0005197	PDE4B phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)
AL136778	0.0000001	DKFZp434J0617 hypothetical protein DKFZp434J0617
D84212	p < 1e-07	STK6 serine/threonine kinase 6
S48196	0.0000007	KAI1 kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody JA4))
AI743249	p < 1e-07	H_GS165L15.1 cAMP response element-binding protein CRE-BPa
BC006376	0.0000001	NMT2 N-myristoyltransferase 2
AK000140	0.0000629	LOC51316 hypothetical protein
AL117410	0.0000003	SVIL supervillin
BC005313	0.0000218	KLK1 kallikrein 1, renal/pancreas/salivary
R42342	0.0000771	EFNB2 ephrin-B2
BC017785	0.0000015	PTPN22 protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
AF068918	p < 1e-07	BIM1 bridging integrator 1
BI792323	0.0000475	LOC51186 pp21 homolog
NM_004038	0.0000731	AMY1A amylase, alpha 1A; salivary
AL035295	0.0000001	H.sapiens gene from PAC-106H8, similar to Dynamain
NM_000935	0.0000159	PLOD2 procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2
AB030000	0.0000805	IL23A interleukin 23, alpha subunit p19
AL049332	p < 1e-07	BTG3 BTG family, member 3
AI827546	0.0000001	ESTs, Highly similar to I39451 amyloid-beta protein [H.sapiens]
BC007836	0.0000005	MDF1 MyoD family inhibitor
AI591051	0.0000002	Homo sapiens, clone IMAGE:4100953, mRNA
NM_001262	0.0000005	CDKN2C cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
AA804433	0.0000182	MX2 myxovirus (influenza virus) resistance 2 (mouse)
BC017901	0.0000307	Homo sapiens, Similar to phospholipid scramblase 1, clone MGC:23806 IMAGE:4253596, mRNA, complete cds
BC001459	0.0000001	RAD51 RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)

AF191771	0.0000084	CED-6 CED-6 protein
AW300933	0.0002531	AQP9 aquaporin 9
AA731110	0.0000001	LOC51185 protein x 0001
AA736984	0.0000004	ADARB1 adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
AI66385	0.000015	SETBP1 SET binding protein 1
BC000612	0.0000021	MGC2599 hypothetical protein MGC2599 similar to katanin p60 subunit A 1 2599
BC015940	0.0000202	NT5 5' nucleotidase (CD73)
AK026589	0.0000043	2-Sep septin 6
AL117485	0.0000865	DKFZp434K191 hypothetical protein DKFZp434K191
AF161398	0.0000012	PRO2013 hypothetical protein PRO2013
BC017498	0.0000018	LOC65243 hypothetical protein
BC008981	0.0000002	MGC9341 similar to RIKEN cDNA 4930500C14 gene
AI970276	0.0000007	KIAA1676 KIAA1676
AA732062	0.0000008	SIAT8D sialyltransferase 8D (alpha-2, 8-polysialyltransferase)
BC014564	0.0000347	MEST mesoderm specific transcript homolog (mouse)
BC003536	0.0006849	MGC10796 hypothetical protein MGC10796
AA861036	0.0000009	ESTs, Weakly similar to T33110 hypothetical protein C18H7.3 - Caenorhabditis elegans [C.elegans]
AF065857	0.0000272	OR7E2P olfactory receptor, family 7, subfamily E, member 2 pseudogene
AF304051	0.0000001	NDRG2 N-myc downstream-regulated gene 2
AL110298	0.0000045	SLC2A3 solute carrier family 2 (facilitated glucose transporter), member 3
AI424406	0.0000004	FLJ14033 hypothetical protein FLJ14033 similar to hypoxia inducible factor 3, alpha subunit
BC009791	0.0000042	HTN3 histatin 3
AL137686	0.0003622	KIAA0855 golgin-67
NM_002451	0.0000014	MTAP methylthioadenosine phosphorylase
BE673992	0.0000187	ESTs
AL136612	0.0000417	NCALD neurocalcin delta
BC001268	0.0000001	NMI N-myc (and STAT) interactor
AF305083	0.0000048	FUT4 fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)
AJ420516	0.0000001	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 966164
AI805080	0.0000002	EST
AA669114	0.0000008	KIAA1842 KIAA1842 protein
AI022925	0.0000167	EMP1 epithelial membrane protein 1
NM_006271	0.0000516	S100A1 S100 calcium binding protein A1
AK055576	0.0000001	MPN marapsin

W46451	0.0000028	LIF leukemia inhibitory factor (cholinergic differentiation factor)
AF217989	0.0000028	PP1665 hypothetical protein PP1665
U66065	0.000005	GRB10 growth factor receptor-bound protein 10
AI245337	0.0001557	HSPB2 heat shock 27kD protein 2
AI969251	0.0000054	RAB7L1 RAB7, member RAS oncogene family-like 1
AW016075	0.0000125	ESTs, Weakly similar to ALUA_HUMAN [HUMAN] ALU CLASS A WARNING ENTRY [H.sapiens]
W60891	0.000027	LGALS7 lectin, galactoside-binding, soluble, 7 (galactin 7)
AF153820	0.0001128	KCNJ2 potassium inwardly-rectifying channel, subfamily J, member 2
NM_006089	0.0001405	SCML2 sex comb on midleg-like 2 (Drosophila)
AI492884	0.0000558	IRF4 interferon regulatory factor 4
NM_006308	0.0000187	HSPB3 heat shock 27kD protein 3
AI632869	0.00004	UPK1B uroplakin 1B
AI821911	0.0000007	ESTs
H06481	0.0000921	KCNK9 potassium channel, subfamily K, member 9 (TASK-3)
NM_001254	0.0000022	CDC6 CDC6 cell division cycle 6 homolog (S. cerevisiae)
BF446419	0.0000022	LOC85414 protein
AL136570	0.000012	LHX6 LIM homeobox protein 6
M62626	0.0000301	HOX11 homeo box 11 (T-cell lymphoma 3-associated breakpoint)
AK025796	0.0002692	LOC55862 uncharacterized hypothalamus protein HCDASE
BF513331	0.0001054	ESTs, Weakly similar to S25689 hypothetical protein hc1 - mouse [M.musculus]
AL117592	0.0000001	EMILIN-2 extracellular glycoprotein EMILIN-2 precursor
BC007348	0.0000024	UP uridine phosphorylase
AA761284	0.0000027	FMR2 fragile X mental retardation 2
X70297	0.0000226	CHRNA7 cholinergic receptor, nicotinic, alpha polypeptide 7
D87119	0.0000128	GS3955 GS3955 protein
AI128198	0.0000516	ESTs
BC016330	0.0000018	PIR51 RAD51-interacting protein
BF510979	0.0000355	DHDH dihydriodol dehydrogenase (dimeric)
AI758745	0.0000001	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
AI467849	0.0000008	TBC1D1 TBC1 (tre-2/JUP6, BUB2, cdc16) domain family, member 1
BC008729	0.0005722	KIAA1309 KIAA1309 protein
BC012328	0.0000048	RPL39L ribosomal protein L39-like
AA588742	0.0000561	XDH xanthine dehydrogenase
M99061	0.0001016	KRT2A keratin 2A (epidermal ichthyosis bullosa of Siemens)

AK024822	0.0000003	ELAC1 elac homolog 1 (E. coli)
BC011393	0.0000597	CHN1 chimerin (chimaerin) 1
AI950844	0.0000171	AIM1L absent in melanoma 1-like
BC007636	0.0000194	C20orf100 chromosome 20 open reading frame 100
BC017401	0.0000342	SERPINB4 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 4
AF414120	0.0001959	CTLA4 cytotoxic T-lymphocyte-associated protein 4
BC002776	0.0000003	SEMA5B sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B
AW014507	0.0000143	KIAA1858 KIAA1858 protein
AI740744	0.0001645	ESTs
X97859	0.0000085	S100A12 S100 calcium binding protein A12 (calgranulin C)
BC013982	0.0000365	KIAA1921 KIAA1921 protein
AK024896	0.0000017	Homo sapiens cDNA: FLJ21243 fis, clone COL01164
BC007079	0.0000158	AF1Q ALL1-fused gene from chromosome 1q
BC007556	0.0000321	Homo sapiens, Similar to TEA domain family member 2, clone MGC:15481 IMAGE:2967735, mRNA, complete cds
AF011333	0.0000364	LY75 lymphocyte antigen 75
M26683	0.0003079	SCYA2 small inducible cytokine A2 (monocyte chemotactic protein 1)
AW151360	0.0000384	TNFSF13B tumor necrosis factor (ligand) superfamily, member 13b
AW131780	0.0005158	NCAM1 neural cell adhesion molecule 1
BM126079	0.000573	ESTs
AF316113	0.0000034	GAL3ST-4 beta-galactose-3-O-sulfotransferase, 4
AF064254	0.0000111	VLCS-H1 VLCS-H1 protein
BC001492	0.0001032	CNTRF ciliary neurotrophic factor receptor
AI200660	0.0000004	ESTs, Weakly similar to T25845 hypothetical protein Y43F4B.7 - Caenorhabditis elegans [C.elegans]
NM_004137	0.0000019	KCNMB1 potassium large conductance calcium-activated channel, subfamily M, beta member 1
AL110257	0.0000839	Homo sapiens mRNA; cDNA DKFZp566P2346 (from clone DKFZp566P2346)
AI096369	0.0004741	ESTs
AL133035	0.0000002	DKFZp434G171 hypothetical protein DKFZp434G171
BM129291	0.0001921	LMO1 LIM domain only 1 (thrombin 1)
AA731866	0.000026	ESTs, Weakly similar to A4584.1 T-complex-associated-testes-expressed-1 protein - mouse [M.musculus]
AL039716	0.0000003	CDC2L2 cell division cycle 2-like 2
AW137630	0.000012	ESTs
AI283926	0.0000099	CSPG4 chondroitin sulfate proteoglycan 4 (melanoma-associated)

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AI445650	0.000064	PRF1 perforin 1 (pore forming protein)
BC005861	0.0000175	ITGB2 integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)
AI927378	0.0000334	H. sapiens cDNA FLJ31267 fis, clone KIDNE2006053, moderately similar to M. musculus mRNA for acetylglucosaminyltransferase-like protein
AI144219	0.0005353	Human l-myc gene exon 3 and 3'-flanking region
AI268609	0.0000005	ESPL1 extra spindle poles like 1 (S. cerevisiae)
AF257182	0.0007686	GPR48 G protein-coupled receptor 48
H17636	0.0000004	GNAL guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type
BC015050	0.0000026	OIP5 Opa-interacting protein 5
AF208043	0.0000872	IFI16 interferon, gamma-inducible protein 16
AB042624	0.0001852	SIRPB2 signal-regulatory protein beta 2
AW014836	0.0000065	ESTs
BC013011	0.000118	MGC2555 hypothetical protein MGC2555
R42108	0.0003179	KIAA0378 KIAA0378 protein
AI371090	0.0000082	KIF3C kinesin family member 3C
BC004295	0.0000105	PTRF polymerase I and transcript release factor
AB017800	0.0004322	NOL4 nucleolar protein 4
BC006458	0.000002	CKS2 CDC28 protein kinase 2
AA883715	0.0000007	ESTs
AF118088	0.0000086	PRO2000 PRO2000 protein
NM_005864	0.0000268	EFS2 signal transduction protein (SH3 containing)
BC009055	0.0001277	FLJ13942 hypothetical protein FLJ13942
AF257238	0.0007241	KIAA1634 KIAA1634 protein
AW451039	0.0000006	FLJ11808 hypothetical protein FLJ11808
AI910678	0.0000136	WASF1 WAS protein family, member 1
AF286095	0.0004553	IL22R interleukin 22 receptor
NM_002497	0.0000048	NEK2 NIMA (never in mitosis gene a)-related kinase 2
NM_006142	0.000009	SFN stratifin
AL136842	0.0002278	CEP3 Cdc42 effector protein 3
AL049443	0.0000451	Homo sapiens mRNA, cDNA DKFZp586N2020 (from clone DKFZp586N2020)
BC006000	0.0000675	MGC12536 hypothetical protein MGC12536
AL133706	0.0001957	ESTs
BF433809	0.0000769	SCYC1 small inducible cytokine subfamily C, member 1 (lymphotactin)

AK025953	0.0001653	Homo sapiens cDNA: FLJ22300 fis, clone HRC04759
AK025428	0.0000283	KIAA0172 KIAA0172 protein
BE858970	0.000055	EST
AA827154	0.0003051	PAG phosphoprotein associated with glycosphingolipid-enriched microdomains
AW512550	0.0004485	ESTs
AA946776	0.0000011	FGF9 fibroblast growth factor 9 (glia-activating factor)
AF018253	0.0000509	TNFRSF11A tumor necrosis factor receptor superfamily, member 11a, activator of NFKB
N32241	0.0003411	Homo sapiens cDNA FLJ32214 fis, clone PLACE6003705
AW293306	0.0001228	K6HF cytokeratin type II
BC000141	0.0001528	MYC v-myc myelocytomatosis viral oncogene homolog (avian)
AF009227	0.0007033	NRG1 neuregulin 1
AI597863	0.0007186	ESTs
AI659900	0.0003695	EST
AW194680	0.0004206	HOXD11 homeo box D11
AA868889	0.0000187	RFP13S ret finger protein-like 3 antisense
BC009352	0.0001185	DKFZp762L0311 hypothetical protein DKFZp762L0311
AW291447	0.0001196	CCR1 chemokine (C-C motif) receptor 1
AK002052	0.0005596	C20orf46 chromosome 20 open reading frame 46
AI446519	0.0000451	ESTs
NM_000734	0.0000771	CD3Z CD3Z antigen, zeta polypeptide (TT3 complex)
NM_032968	0.0000017	PCDH11 protocadherin 11
BF509016	0.0000177	Homo sapiens cDNA FLJ30899 fis, clone FEBRA2005726
M93426	0.0000025	PTPRZ1 protein tyrosine phosphatase, receptor-type, Z polypeptide 1
AK026663	0.0000204	FLJ21034 hypothetical protein FLJ21034
BF433635	0.0000216	ESTs
AF104313	0.0002268	ESDN endothelial and smooth muscle cell-derived neuropilin-like protein
BC000356	0.0000032	MAD2L1 MAD2 mitotic arrest deficient-like 1 (yeast)
AI625086	0.0000526	FLJ11585 hypothetical protein FLJ11585
AI560377	0.0003146	ESTs
BF112041	0.0000027	KIAA0401 KIAA0401 protein
AI831078	0.0003873	ESTs, Weakly similar to CA18 MOUSE COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR [M.musculus]
AF007194	0.0000116	MUC3A mucin 3A, intestinal
NM_000436	0.0000291	OXCT 3-oxoacid CoA transferase
BC007828	0.0000485	MGC14128 hypothetical protein MGC14128

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AF396928	0.000446	EPST11 epithelial stromal interaction 1 (breast)
U43203	0.0004703	TTF1 thyroid transcription factor 1
BC000012	0.0002624	GFP2 glutamine-fructose-6-phosphate transaminase 2
AF047711	0.0000029	RASA2 RAS protein activator like 2
AF053453	0.0001192	TM4SF6 transmembrane 4 superfamily member 6
BC017054	0.0000027	MTF1D2 methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase
AI769930	0.0000068	Homo sapiens (clone B3B3E13) Huntington's disease candidate region mRNA fragment
BC002914	0.0000453	WASPIP Wiskott-Aldrich syndrome protein interacting protein
BE671403	0.0004777	ESTs
AI249782	0.0001099	PPP4F2 protein phosphatase 4 regulatory subunit 2
AJ420537	0.0000104	dJ55C23.6 dJ55C23.6 gene
AI239743	0.0001411	LTA lymphotoxin alpha (TNF superfamily, member 1)
NM_001890	0.0003456	CSN1 casein, alpha
AF303058	0.0000457	NP25 neuronal protein
BC004336	0.0000035	MGC10946 hypothetical protein MGC10946
AI590055	0.0000213	ESTs
AW301017	0.0001513	ESTs
BC015497	0.0000283	TEAD4 TEA domain family member 4
BC008483	0.0000566	SERP1NB3 serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 3
BC007072	0.0000858	MGC12538 hypothetical protein MGC12538
AI384087	0.0001257	KIAA0603 KIAA0603 gene product
AB023135	0.000755	ICOS inducible T-cell co-stimulator
AB023967	0.0000858	ROD1 ROD1 regulator of differentiation 1 (S. pombe)
AI560576	0.0006927	PTPRK protein tyrosine phosphatase, receptor type, K
AK024951	0.0000497	C1R complement component 1, r subcomponent
AW452231	0.0004972	CD244 natural killer cell receptor 2B4
AK027515	0.0000623	Homo sapiens CDNA FLJ14609 fts, clone NT2RP1000944
AL043170	0.0001136	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
AK025636	0.0001079	Homo sapiens CDNA FLJ21983 fts, clone HEP06219
NM_006278	0.0000121	SIAT4C sialyltransferase 4C (beta-galactosidase alpha-2,3-sialyltransferase)
BC003388	0.0001059	TANK TRAF family member-associated NFKB activator
AA777592	0.0005802	ESTs, Weakly similar to ubiquitous TPR motif, Y isoform [H.sapiens]
BC016623	0.0000111	ETV4 ets variant gene 4 (E1A enhancer binding protein, E1AF)

022041001010PC		
BC005408	0.0000236	FLJ23119 hypothetical protein FLJ23119
AF233588	0.0001101	LOC51285 RIs
BC018644	0.0001366	NUD18 nudix (nucleoside diphosphate linked moiety X)-type motif 8
AW057670	0.0000078	ESTs, Weakly similar to S55824 reverse transcriptase homolog [H.sapiens]
AF414088	0.000153	COL21A1 collagen, type XXI, alpha 1
X96757	0.0001749	MAP2K6 mitogen-activated protein kinase kinase 6
NM_005965	0.0002044	MYLK myosin, light polypeptide kinase
R40207	0.00041	PIP5K1B phosphatidylinositol-4-phosphate 5-kinase, type I, beta
AK026315	0.0005265	FLJ22662 hypothetical protein FLJ22662
AK025130	0.0000064	FLJ21477 hypothetical protein FLJ21477
BC014444	0.0000298	ASML3B acid sphingomyelinase-like phosphodiesterase
AJ012214	0.0000751	11-Oct POU transcription factor
AL137343	0.0000089	Homo sapiens mRNA for putative NSE I protein
AK024855	0.0000346	CTSS cathepsin S
BC002727	0.0001627	SDCBP2 syndecan binding protein (syntenin) 2
AK026337	0.0000268	FLJ22684 hypothetical protein FLJ22684
AK025346	0.0009842	Homo sapiens cDNA: FLJ21693 fis, clone COL09609
AI536895	0.0001916	LOX lysyl oxidase
AF339783	0.0004293	FLJ20159 hypothetical protein FLJ20159
AB038781	0.0000178	MUC3B mucin 3B
BC011969	0.0001809	Homo sapiens, clone IMAGE:3880654, mRNA
AF326964	0.0001063	BCL2L10 BCL2-like 10 (apoptosis facilitator)
AF033347	0.0004868	KCNQ3 potassium voltage-gated channel, KQT-like subfamily, member 3
AF070631	0.0000349	TMPO thymopoietin
BC015507	0.000679	CST7 cystatin F (leukocystatin)
AI811072	0.000041	VEGF VEGF nerve growth factor inducible
BC006346	0.000113	APEG1 nuclear protein, marker for differentiated aortic smooth muscle and down-regulated with vascular injury
AF247167	0.0001179	AD031 AD031 protein
L27711	0.0001896	CDKN3 cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)
AA810577	0.0000119	ARSB arylsulfatase B
AF328296	0.0000516	FLJ14437 myopalladin
AI147926	0.0001123	CSF2RB colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)
AF017988	0.00017	SFRP5 secreted frizzled-related protein 5
AI151185	0.0000495	LHPP phospholysine phosphohistidine inorganic pyrophosphate phosphatase

022041001010PC		
AW271272	0.0000564	FOXG2 forkhead box C2 (MFH-1, mesenchyme forkhead 1)
BI324932	0.0000637	PTGER4 prostaglandin E receptor 4 (subtype EP4)
AF105378	0.00025	HS3ST4 heparan sulfate (glucosamine) 3-O-sulfotransferase 4
BC009642	0.0000406	FXYD5 FXYD domain-containing ion transport regulator 5
BF002341	0.0000493	ESTs, Moderately similar to AF174605 1 F-box protein Fbx25 [H.sapiens]
H06160	0.0001828	C1orf17 chromosome 1 open reading frame 17
NM_001839	0.0000549	CNN3 calponin 3, acidic
BC015397	0.0001164	Homo sapiens, Similar to RIKEN cDNA 4921507P07 gene, clone MGC:21710 IMAGE:4448480, mRNA, complete cds
AK026144	0.0006923	TEL2 transcription factor ets
BC008749	0.0000146	MBP myelin basic protein
BC007678	0.0000353	ADA adenosine deaminase
AA814043	0.0004392	ESTs
AW291196	0.0001248	ESTs
AI090561	0.0005695	M160 scavenger receptor cysteine-rich type 1 protein M160 precursor
AF098066	0.0000203	SART-2 squamous cell carcinoma antigen recognized by T cell
AK025615	0.0001353	Homo sapiens cDNA: FLJ21962 fls. clone HEP05564
AU152414	0.0004928	DNAH11 dynein, axonemal, heavy polypeptide 11
U49395	0.0006226	P2RX5 purinergic receptor P2X, ligand-gated ion channel, 5
AI611312	0.0002789	KIAA0942 KIAA0942 protein
AI689069	0.0001012	CORO1A coronin, actin binding protein, 1A
AF117386	0.0000326	USP1 ubiquitin specific protease 1
NM_001452	0.0001101	FOXF2 forkhead box F2
AI025919	0.0000271	ESTs
AF225416	0.0000275	AD024 AD024 protein
AA910331	0.0006572	COL4A1 collagen, type IV, alpha 1
AA743321	0.0000364	ESTs
AI290556	0.0000413	ESTs
BE676183	0.0002021	KIAA1798 KIAA1798 protein
AA831508	0.0008458	ESTs
BC012945	0.0000572	MGC11271 hypothetical protein MGC11271
BC004278	0.0000617	FLJ23239 hypothetical protein FLJ23239
BC004267	0.0001122	MGC10818 hypothetical protein MGC10818
AW449550	0.0001866	GAP1P4BP RAS p21 protein activator (GTPase activating protein) 3 (Ins(1,3,4,5)P4-binding protein)

BC000049	0.0002093	FLJ10493 hypothetical protein FLJ10493
R56080	0.0003624	RELN reelin
AF039655	0.0000292	BFSP1 beaded filament structural protein 1, filensin
A1656630	0.0002032	TMEM7 transmembrane protein 7
AW411170	0.0003073	EAf1 EAF1 protein
A1280476	0.0004985	APG-1 heat shock protein (hsp110 family)
BF510271	0.0000551	LOC51063 hypothetical protein
BC007533	0.0001578	NRP1 neuropilin 1
A1671448	0.00021	ESTs
U62824	0.0009236	H.sapiens mRNA for HLA-C alpha chain (Cw*1701)
AF025887	0.0000808	GSTA4 glutathione S-transferase A4
BF513346	0.0004176	ESTs
AW452418	0.0006057	RYR2 ryanodine receptor 2 (cardiac)
AL117401	0.0006587	DKFZP434P211 DKFZp434P211 protein
AF324830	0.0007875	ILT11 leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 7
BC004291	0.0000444	KIAA0080 KIAA0080 protein
AF223943	0.0000452	GLS glutaminase
AK000626	0.000305	FLJ20619 hypothetical protein FLJ20619
A1766890	0.0008599	ESTs, Weakly similar to NAH6_HUMAN SODIUM/HYDROGEN EXCHANGER 6 [H.sapiens]
BM141806	0.0002858	Homo sapiens cDNA FLJ30365 fis, clone FEBRA2004099
Y13786	0.0001617	ADAM19 a disintegrin and metalloproteinase domain 19 (meltin beta)
BF508503	0.0000643	Homo sapiens cDNA FLJ32102 fis, clone OCBBF2001196
AW073971	0.0000986	ESTs, Weakly similar to T00705 N-chimerin homolog F25965_3 [H.sapiens]
M87507	0.0002201	CASP1 caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)
AJ315514	0.000686	NR3C2 nuclear receptor subfamily 3, group C, member 2
A1240521	0.0002527	CHML choroideremia-like (Rab escort protein 2)
NM_057749	0.0003057	CCNE2 cyclin E2
BC012113	0.000344	HOMER-3 Homer, neuronal immediate early gene, 3
BE551149	0.0005021	ESTs
AW081673	0.0000873	SAH SA hypertension-associated homolog (rat)
AB016901	0.0001215	HGC6.2 HGC6.2 protein
BC006093	0.0001312	MMP9 matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase)
NM_000795	0.000318	DRD2 dopamine receptor D2
AA630788	0.000387	TOP2A topoisomerase (DNA) II alpha (170kD)

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AL137274	0.000862	MIG-6 Gene 33/Mig-6
U89995	0.0001892	FOXEl forkhead box E1 (thyroid transcription factor 2)
M85294	0.0002409	PRKR protein kinase, interferon-inducible double stranded RNA dependent
BC003097	0.0000678	ICAM2 intercellular adhesion molecule 2
AL137346	0.0000816	Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)
AK027138	0.0000856	KIAA0914 KIAA0914 gene product
BC009628	0.0000828	Homo sapiens, clone IMAGE:3898148, mRNA, partial cds
AB037715	0.0002083	FLJ10210 hypothetical protein FLJ10210
AW084130	0.0008664	NOS3 nitric oxide synthase 3 (endothelial cell)
AA807955	0.0002328	EST
AK024697	0.0007384	FLJ21044 hypothetical protein FLJ21044 similar to Rbig1
AL137662	0.0002524	Homo sapiens mRNA; cDNA DKFZp434P086 (from clone DKFZp434P086); partial cds
AI732321	0.0001257	ESTs
AL137506	0.0007917	FLJ23563 hypothetical protein FLJ23563
R43523	0.0005701	FLJ22202 hypothetical protein FLJ22202
AI869243	0.0003403	ESTs
AW291368	0.0002584	ESTs, Weakly similar to KIAA0738 protein [H.sapiens]
BC001350	0.0009786	ARG2 arginase, type II
AK022735	0.0001058	FLJ12673 hypothetical protein FLJ12673
BF510331	0.0001294	MCM3AP MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) associated protein
AL136703	0.0004855	DKFZP566J091 hypothetical protein DKFZp566J091
AI953054	0.0001233	TKT transketolase (Wernicke-Korsakoff syndrome)
BC014317	0.0002587	NX-17 kidney-specific membrane protein
BC014890	0.0004285	SLUG slug homolog, zinc finger protein (chicken)
BC001645	0.000697	SYK spleen tyrosine kinase
AI188578	0.0002173	FLJ11036 hypothetical protein FLJ11036
AI733497	0.0005164	ESTs
AW293496	0.00068	ESTs
AF269223	0.0005681	TCP11 t-complex 11 (mouse)
AB012643	0.0006384	ALPL alkaline phosphatase, liver/bone/kidney
U75309	0.0006677	TAF5 TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100 kD
NM_015901	0.0001783	LOC51055 unknown
AK021801	0.0002326	Homo sapiens cDNA FLJ11739 fis, clone HEMBA1005497
AW295061	0.0002448	WSX1 class I cytokine receptor

022041001010PC

AI559983	0.0004987	CDC2 cell division cycle 2, G1 to S and G2 to M
BC015496	0.000254	INPP1 inositol polyphosphate-1-phosphatase
X93595	0.0002125	KIR3DL2 killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2
		Homo sapiens cDNA FLJ30999 fis, clone HLUNG1000110, weakly similar to PISTIL-SPECIFIC EXTENSIN-LIKE
AI765908	0.0005868	PROTEIN PRECURSOR
NM_005923	0.00086	MAP3K5 mitogen-activated protein kinase kinase 5
BC016757	0.0002739	SAP30 sin3-associated polypeptide, 30kD
AK027121	0.0002624	FLJ23468 hypothetical protein FLJ23468
BE644686	0.0005227	KIAA0509 KIAA0509 protein
AI418207	0.0007707	ESTs
		Homo sapiens, Similar to RNA polymerase I transcription factor RRN3, clone MGC:15321 IMAGE:3678732,
BC009198	0.0004215	mRNA, complete cds
AA761502	0.0005644	KIAA0009 KIAA0009 gene product
BC018112	0.0005867	PROL2 proline rich 2
BC002718	0.000673	FN14 type I transmembrane protein Fn14
AL353948	0.0009563	Homo sapiens mRNA; cDNA DKFZp761P0114 (from clone DKFZp761P0114)
AK023806	0.0009698	FLJ13744 hypothetical protein FLJ13744
AI264615	0.0007686	SIRT4 sirtuin silent mating type information regulation 2 homolog 4 (S. cerevisiae)
BC002715	0.0007069	PPARD peroxisome proliferative activated receptor, delta
M96843	0.0007716	ID2B striated muscle contraction regulatory protein
BC007289	0.0008457	ARPM1 actin related protein M1
AI338498	0.0008464	ZNF295 zinc finger protein 295
W46976	0.0009251	EST

Table 5

GenBank accession	CloneID	UnigeneID			
AW473119	725321	Hs.1657	NM_003508	2149968	Hs.158335
AW015443	841621	Hs.100686	BC017859	298417	Hs.82961
NM_001218	594633	Hs.5338	NM_000352	1558108	Hs.54470
AF131785	2284924	Hs.90419	AA804407	325515	Hs.29716
AJ009985	239568	Hs.279928	AF176012	120138	Hs.260720
AF088867	2321113	Hs.91011	AF052504	26294	Hs.241471
AF007153	726703	Hs.7888	AI263695	502173	Hs.72050
BC014948	1558642	Hs.321130	AW139831	258167	Hs.284186
AA542898	762668	Hs.33846	AA156097	969843	Hs.29283
AA569340	1631209	Hs.330780	BC006428	139354	Hs.15093
AW137092	1554430	Hs.94694	AK024872	487932	Hs.92254
NM_005080	725968	Hs.149923	AK024872	826194	Hs.92254
BC006793	214068	Hs.169946	BC016861	590310	Hs.351461
NM_004496	1610546	Hs.299867	AI272823	83358	Hs.76704
U95089	137017	Hs.77432	AI674226	279720	Hs.125201
U95089	183468	Hs.77432	AI373462	155072	Hs.29190
AJ404611	1584563	Hs.130881	AK000978	505575	Hs.79741
AI128582	1691237	Hs.190642	AA807457	243549	Hs.1334
NM_020974	242778	Hs.222399	AL133622	1571106	Hs.301011
AI332979	2321529	Hs.118695	R49089	179212	Hs.24811
AA688021	111389	Hs.179808	AJ420423	593431	Hs.23703
AI820662	1607198	Hs.129598	BC017352	377275	Hs.82237
AI125908	51185	Hs.125019	U62325	1470333	Hs.324125
AK026818	69378	Hs.279898	AI804588	1733262	Hs.167380
BC014962	1700429	Hs.105445	AI733682	1637829	Hs.130239
AW024203	530197	Hs.349344	BC012372	868652	Hs.278625
AL137566	504959	Hs.32405	AF007170	1492468	Hs.125783
AI874215	299332	Hs.193914	BC007008	839736	Hs.1940
BC013732	66599	Hs.155956	BC013438	1640821	Hs.42792
R41823	1558233	Hs.7413	BC017733	1909775	Hs.349227
AK000442	1562618	Hs.11408	BC017733	877772	Hs.349227
AK025256	1632235	Hs.129691	AY029179	753198	Hs.333893
NM_006763	213136	Hs.75462	AF271781	471196	Hs.111577
NM_006763	71428	Hs.75462	BC007681	1911343	Hs.3797
NM_001238	68950	Hs.9700	H29323	270917	Hs.7306
BC011348	785795	Hs.15929	AY043361	813281	Hs.324275
N31940	866488	Hs.14434	AF070632	669359	Hs.23729
BC014601	839382	Hs.88417	NM_004310	302591	Hs.109918
AF356492	431003	Hs.63931	BE967259	342181	Hs.79241
BC012375	179212	Hs.279937	NM_000044	2250839	Hs.99915
BC012375	767289	Hs.279937	AI823785	782497	Hs.6349
GenBank accession	CloneID	UnigeneID	BC012914	592832	Hs.180059
AI200852	1836699	Hs.127780	AF084830	1901562	Hs.127007
AA130089	490965	Hs.23136	AI637899	2237353	Hs.1907
AA255953	243100	Hs.81934	AL110126	813265	Hs.326416
NM_012244	415670	Hs.22891	AF033021	756708	Hs.10082
			AA749341	814054	Hs.158282
			BC000558	647397	Hs.101174
			AI364725	809779	Hs.9729
			X70340	1553998	Hs.170009

AI471793	415550	Hs.60257	NM_004938	2043415	Hs.153924
BC017701	823655	Hs.21941	AW206460	454632	Hs.6360
NM_014599	730288	Hs.55058	BC018035	1557994	Hs.127043
AA659816	795851	Hs.23830	BC014189	854763	Hs.10260
AA622986	731047	Hs.104830	BF433570	1557637	Hs.144479
AI871614	344959	Hs.58241	BC008915	1323591	Hs.76353
AK026946	220395	Hs.27099	AA806280	772913	Hs.349306
AA761512	783698	Hs.81412	AI140061	304908	Hs.1189
AL136579	219929	Hs.109315	AI828071	1616253	Hs.129057
AW574736	261541	Hs.143460	AF269101	796539	Hs.27695
AI337740	41569	Hs.4243	AW294316	1847093	Hs.125608
AI382972	773170	Hs.82128	AF104032	1702742	Hs.184601
AJ249248	685516	Hs.97101	AF104032	755578	Hs.184601
BC013300	531319	Hs.180655	BC013430	139835	Hs.28309
AA587049	2494805	Hs.211587	BC008317	52933	Hs.79136
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AW204371	293689	Hs.239727	BC009211	125788	Hs.8739
AB023430	2019426	Hs.156114	AI351524	796197	Hs.169470
AW136298	2449841	Hs.3185	AF153605	1554009	Hs.107528
AL117452	767068	Hs.44155	BC017758	724888	Hs.687
NM_014211	563598	Hs.70725	NM_007210	470964	Hs.151678
AA845338	197525	Hs.14286	AF131789	32489	Hs.4863
AI741657	683569	Hs.198443	BI492630	20115	Hs.62185
AW195038	2017930	Hs.129867	BC017918	868396	Hs.302766
AK000012	1517212	Hs.184634	AL080192	2312454	Hs.101282
BF434467	82869	Hs.11805	AF091092	768007	Hs.43728
BC005395	1854648	Hs.346935	AW207201	1507713	Hs.97220
BC005395	85468	Hs.346935	BC001283	416959	Hs.33267
AA767129	310034	Hs.56336	NM_005401	2390593	Hs.159238
AB022918	272706	Hs.34578	NM_007050	41647	Hs.225952
AA648922	127510	Hs.1634	BC003610	785744	Hs.3745
AF026477	1536215	Hs.6079	AI631667	344073	Hs.351344
AJ420468	1901310	Hs.51965	S72493	1486533	Hs.115947
AA775255	2299609	Hs.284163	AF193809	1456468	Hs.279682
BC018646	204897	Hs.75648	BC012107	391949	Hs.103527
BC010626	214205	Hs.28149	X83301	470261	Hs.324728
AL161952	1609836	Hs.170171	BC002738	1323448	Hs.17409
AI095049	1686314	Hs.6786	BE464993	2062533	Hs.112158
AK055698	1860909	Hs.349189	BG272534	289505	Hs.44829
AI261967	377252	Hs.45743	R50991	1586124	Hs.12247
H10667	80727	Hs.274243	AF117108	429494	Hs.79440
AK025347	415766	Hs.170162	AL157505	32050	Hs.21380
BC000088	137940	Hs.2006	N22687	266500	Hs.8236
BC003628	1486082	Hs.1690	AJ278018	1637767	Hs.12079
BE965331	2309234	Hs.87417	AW294857	25274	Hs.21050
AI432615	785745	Hs.264	AI804716	544639	Hs.95612
AF100759	416374	Hs.284243	NM_004923	1518890	Hs.121378
R15881	2118505	Hs.7138	AA177001	809674	Hs.112184

BC009722	1637893	Hs.105887	BC006168	840333	Hs.82432
BC000703	292936	Hs.48855	BC005910	346688	Hs.279651
Z73678	1662279	Hs.198382	BC008682	726582	Hs.12887
BC007595	1558675	Hs.44317	BF446789	1946448	Hs.139851
BC009203	212456	Hs.25925	BF446789	840984	Hs.139851
AF132818	132711	Hs.84728	AB050468	1533710	Hs.4193
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BF110928	1556859	Hs.126932	AI126271	488202	Hs.49433
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AK026420	1161564	Hs.10587	AW194426	1518845	Hs.20726
AI567843	51078	Hs.349090	BC001940	66406	Hs.104659
AK025562	418049	Hs.18612	R42732	214996	Hs.283705
AL080079	786695	Hs.44197	AA716439	1898758	Hs.99824
BC002660	723986	Hs.170453	AI202593	2119039	Hs.144877
BC008764	742798	Hs.69360	BF511352	193913	Hs.80887
AL137311	281392	Hs.234074	BC009373	1635059	Hs.326391
BI493178	415191	Hs.78894	NM_006769	1706027	Hs.3844
AF181862	2016775	Hs.242407	X55362	796646	Hs.75212
BC010039	144849	Hs.289092	AI636974	811774	Hs.238126
BE326342	155532	Hs.129043	AI494546	307255	Hs.10649
NM_004419	342378	Hs.2128	AJ420562	26883	Hs.106106
BC000881	2017415	Hs.1594	BC015338	2063284	Hs.180884
AI498405	754346	Hs.34145	AL050227	784178	Hs.27860
AL137332	754157	Hs.23869	BF433019	950355	Hs.110080
AI367357	255285	Hs.112083	AK025296	204790	Hs.95549
AB048286	161484	Hs.334305	AA088779	1635970	Hs.24724
AL110139	1844765	Hs.27373	AA846278	51700	Hs.5740
BC014913	786663	Hs.247525	BI495988	626841	Hs.285754
AB018329	897731	Hs.24212	BI495988	754509	Hs.285754
AF038191	51097	Hs.134846	AI150439	208387	Hs.15370
AF043473	249687	Hs.117780	AI732309	153760	Hs.78436
AK057601	752903	Hs.54985	BC006526	810873	Hs.2794
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BC012844	812048	Hs.74621	AF089854	1947911	Hs.8022
AL512749	752625	Hs.93961	AA714213	66406	Hs.352002
BC011721	757489	Hs.349695	AY007114	296679	Hs.44898
NM_001793	773301	Hs.2877	N89991	772962	Hs.44070
AI273928	814798	Hs.75746	BC000576	23776	Hs.75438
Y17978	1968246	Hs.118722	BE672557	282980	Hs.42640
BC004143	741977	Hs.69771	BC015525	809784	Hs.79361
AI694966	490178	Hs.49597	AL136539	768068	Hs.169333
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U74612	564803	Hs.239	BC017338	308437	Hs.576
BC007609	2112387	Hs.231444	D50840	812196	Hs.152601
AL117633	190325	Hs.348724	BC017575	246524	Hs.20295
AF222980	767471	Hs.26985	BC012089	27544	Hs.112360
AI678454	2052032	Hs.61638	AJ420473	797038	Hs.7869
BC000809	786607	Hs.95243	M57892	823718	Hs.100322
BC014213	746373	Hs.159505	AI436812	1553560	Hs.143640

M57609	767447	Hs.72916	BC008832	782811	Hs.139800
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AI797041	382787	Hs.182231	AI631708	1048592	Hs.121554
AI741143	767164	Hs.235857	NM_002852	1691868	Hs.2050
BC001766	759948	Hs.83384	BC016004	840466	Hs.67726
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NM_006006	2499829	Hs.37096	AI278360	1655480	Hs.31409
U97105	841620	Hs.173381	AB040057	254029	Hs.23643

AI538226	1911864	Hs.32976	AW082270	1895781	Hs.12496
AW340797	773152	Hs.98434	AW082270	52071	Hs.12496
AW006452	366526	Hs.58006	AI499593	152453	Hs.25351
AF116660	50562	Hs.283683	AA053400	127063	Hs.203213
AI199268	511096	Hs.19322	AF016267	110226	Hs.119684
AF051152	80633	Hs.63668	AL119854	361587	Hs.296317
AA857853	302127	Hs.204238	BC014277	489519	Hs.245188
R38689	35812	Hs.12376	AL110124	502446	Hs.5297
AA883715	1461550	Hs.125494	BF447150	1556897	Hs.119383
AL043469	785975	Hs.80424	AF218006	2297394	Hs.24391
AL360254	46843	Hs.30965	AW450080	241043	Hs.322149
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S48196	1474284	Hs.323949	AJ223366	1915759	Hs.116051
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AB032698	1722980	Hs.14770	BF436849	1499900	Hs.8917
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AW189851	488956	Hs.211610	BC008584	344430	Hs.170195
AL096842	744395	Hs.7946	BF509554	1842331	Hs.144921
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AK027191	510273	Hs.240443	BC008857	725649	Hs.77810
AI283489	2014138	Hs.154890	U96136	51083	Hs.80220
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X53587	811096	Hs.85266	AW732240	22500	Hs.16365
AK026181	2012257	Hs.288850	M93426	785148	Hs.78867
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BC001844	41358	Hs.104105	AL080059	745011	Hs.173094
AI921122	1504268	Hs.148218	BF196234	1884217	Hs.147491
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H08145	48033	Hs.23606	U87460	41658	Hs.27747
NM_001078	44477	Hs.109225	AI469557	813520	Hs.2913
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NM_005409	1030351	Hs.103982	L10386	301735	Hs.2022
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AI335013	417884	Hs.237642	AB028967	770427	Hs.202687
BC017785	1638481	Hs.87860	BC000356	814701	Hs.79078
AI767898	841492	Hs.237809	NM_033014	629906	Hs.109439

AA883246	782537	Hs.131740	X97859	342458	Hs.19413
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U63008	1649374	Hs.15113	NM_006103	786675	Hs.2719
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AA805970	726678	Hs.74583	AL137343	177665	Hs.260855
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AI383975	868168	Hs.11261	NM_006142	2027515	Hs.184510
AA668884	124128	Hs.19155	BC007659	813387	Hs.80706
NM_006186	898221	Hs.82120	AA854341	186301	Hs.38034
AL080078	322511	Hs.85335	AI797308	194638	Hs.193651
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AL157455	31299	Hs.22543	NM_014279	52076	Hs.74376
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NM_003155	565075	Hs.25590	AI283926	40056	Hs.9004
BC007921	295093	Hs.192861	AI373939	839101	Hs.74471
AK026589	143966	Hs.90998	AW207140	363590	Hs.6111
AL110298	202201	Hs.7594	BC004295	767993	Hs.29759
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AI569068	812294	Hs.22247	AI026838	280763	Hs.30120
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BC010691	321455	Hs.343553	AF161505	788524	Hs.99291
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AW014836	415326	Hs.18844	AI910678	284734	Hs.75850
BC014651	773296	Hs.98428	AF085233	261609	Hs.279696
AF023676	2020772	Hs.31130	AF085233	3316104	Hs.279696
AF063020	745118	Hs.82110	BC018127	140806	Hs.83920
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AL161983	502096	Hs.21415	AK025624	1637791	Hs.71331
AI125473	2029503	Hs.157281	AK025624	587992	Hs.71331
BC008036	344588	Hs.50915	AF119815	788698	Hs.99231
AI371090	784257	Hs.21611	AW139237	796480	Hs.30875

AI656385	1562231	Hs.151717	AK024750	726860	Hs.32017
AA613425	2062432	Hs.1584	M62626	429368	Hs.89583
BC001969	595162	Hs.301198	BC017901	489320	Hs.292358
BC001207	841057	Hs.7457	AF117386	1581685	Hs.35086
AL110252	49204	Hs.168950	AA747541	1526789	Hs.300592
AA761787	49482	Hs.315482	AK024855	687875	Hs.181301
BC007079	812105	Hs.75823	BC014564	898219	Hs.79284
F10094	22428	Hs.333319	AF070631	1500821	Hs.11355
NM_000935	263013	Hs.41270	AF070631	454083	Hs.11355
AA910336	1520559	Hs.135186	AF070631	79761	Hs.11355
U67784	246786	Hs.23016	BC007678	505881	Hs.1217
AI022925	1589468	Hs.79368	BC000632	530035	Hs.14331
BC008283	258790	Hs.80247	BC005963	1631546	Hs.36978
NM_003122	1412481	Hs.181286	AA233494	2284619	Hs.159468
AA804433	701481	Hs.926	BE549691	1860836	Hs.244391
BC017772	289057	Hs.47166	L02785	1873533	Hs.1650
NM_006308	2088978	Hs.41707	AW151360	593690	Hs.270737
BE673992	1584638	Hs.128211	AW118445	175103	Hs.57652
AA868889	1638827	Hs.274285	BC009799	1410444	Hs.270833
AL157471	33837	Hs.15420	R40176	27769	Hs.167406
X59766	1456160	Hs.71	AL136612	768520	Hs.90063
BC007636	41332	Hs.26608	AL136612	838478	Hs.90063
AI566899	753034	Hs.35841	AA600175	230560	Hs.39720
AA910884	1520895	Hs.130217	BC004291	780937	Hs.74554
BC015940	42070	Hs.153952	NM_001197	1916575	Hs.155419
NM_030761	1909317	Hs.302428	AW207696	2250736	Hs.97644
AI590055	1523411	Hs.124110	BC002914	700299	Hs.24143
NM_004425	301122	Hs.81071	R61469	53122	Hs.281587
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BF433635	1911471	Hs.145711	AF303058	325160	Hs.169330
BC005313	1705861	Hs.123107	AI248610	110578	Hs.15060
AL133591	2016924	Hs.141480	U31214	588460	Hs.301350
AI362949	2019009	Hs.75169	AK024951	83549	Hs.1279
AF334710	78946	Hs.8364	NM_013267	1911706	Hs.325443
AL161961	1500766	Hs.17767	BC000006	897950	Hs.78629
AF094754	155038	Hs.32973	BC004471	740941	Hs.74120
AF094754	1685363	Hs.32973	AK025062	564801	Hs.172129
AK026760	75059	Hs.251946	NM_006271	179046	Hs.292707
AF052224	2432360	Hs.194684	NM_001839	486787	Hs.194662
NM_005864	795730	Hs.24587	BF510271	2049813	Hs.241545
AW205768	2300372	Hs.91877	AB067468	85660	Hs.11006
AW139532	814154	Hs.105069	AI492884	1358229	Hs.82132
AI025919	1757930	Hs.131674	AA588742	127709	Hs.250
AF065857	2809853	Hs.248185	AW271272	2769084	Hs.239571
AL136678	1455603	Hs.87729	BC008483	727147	Hs.227948
AK025428	812975	Hs.77546	BF434466	32493	Hs.227730
BC015497	346696	Hs.94865	NM_002963	1088345	Hs.112408
AI272951	85643	Hs.75599	NM_002988	768497	Hs.16530
NM_000436	28469	Hs.177584	BC011393	898258	Hs.169965
AI697249	1566793	Hs.784	BC009753	1635307	Hs.234898

BC004278	1417886	Hs.34516	J03607	810131	Hs.182265
AK025307	1554646	Hs.259785	AL043170	758284	Hs.160881
AK000140	491644	Hs.107139	NM_005410	530814	Hs.3314
BI324932	363569	Hs.199248	BC015397	1908705	Hs.122055
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AL039118	33051	Hs.2714	AF053453	252382	Hs.121068
M84757	813614	Hs.1076	AA923424	289025	Hs.135567
BC003097	130201	Hs.347326	AW291447	472008	Hs.301921
NM_001792	325182	Hs.161	AA999861	1636369	Hs.126892
R92436	196305	Hs.131837	AI953054	530875	Hs.89643
BF001174	487297	Hs.296341	BC002591	1384851	Hs.2258
BC006267	1524001	Hs.7331	AI384087	753162	Hs.173802
BC005257	2251833	Hs.183752	AI732321	154795	Hs.348819
NM_004038	809998	Hs.274376	BF510331	203896	Hs.168481
AK055386	365991	Hs.285050	BC006093	22040	Hs.151738
AJ012214	2191807	Hs.227115	BC006378	250883	Hs.16695
U06641	78294	Hs.150207	BF510778	898058	Hs.53997
BF433809	1896981	Hs.3195	AF146761	288807	Hs.20450
NM_000734	1572298	Hs.97087	AI239743	345232	Hs.36
R42342	796198	Hs.30942	BM127823	1584449	Hs.294151
NM_002514	1505534	Hs.235935	BM127823	786525	Hs.294151
AI280246	1893765	Hs.149504	AB041036	740780	Hs.57771
AF025887	504791	Hs.169907	AI962213	1467799	Hs.22599
AL137346	22917	Hs.13299	AF068180	1565079	Hs.167746
NM_004370	786609	Hs.101302	AW301017	1712825	Hs.146492
BC009628	1569815	Hs.127771	AI241077	461727	Hs.1870
AF059321	1610146	Hs.301698	BC000141	812965	Hs.79070
BC010652	415589	Hs.91668	AI245337	1870305	Hs.78846
AW291180	1455566	Hs.258	BC014533	1908758	Hs.44268
AF208043	824602	Hs.155530	R43793	50615	Hs.80288
AW081673	296529	Hs.181345	BC007533	489535	Hs.69285
D50419	1404841	Hs.119014	AA973836	1586043	Hs.128739
AF034996	44164	Hs.173034	Y13786	1557714	Hs.278679
AW448954	490784	Hs.143046	BC002727	1555478	Hs.64179
AI741469	1732247	Hs.57787	AI740744	22773	Hs.10475
NM_003248	758266	Hs.75774	AK025953	126341	Hs.288965
AW073971	345234	Hs.238954	BC005989	1874603	Hs.143113
AI689069	487988	Hs.109606	X96757	45578	Hs.118825
BC015947	2138030	Hs.47584	R45048	29954	Hs.159538
BC003388	502486	Hs.146847	BC015613	135688	Hs.334695
AL117616	280950	Hs.300741	BC011969	771004	Hs.347534
BC005246	509731	Hs.84072	H06160	1519985	Hs.106794
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AF233588	1614140	Hs.27018	AF102848	454970	Hs.9029
NM_001452	310138	Hs.44481	L27711	700792	Hs.84113
BF512918	2363954	Hs.2159	AF030186	358217	Hs.58367
AI311775	2046679	Hs.192819	AI536895	248829	Hs.102267
NM_006455	347434	Hs.207251	BM129291	2017950	Hs.1149
BC004267	950451	Hs.135200	AL133706	283748	Hs.4257
AI147926	141115	Hs.285401	BE676183	1670836	Hs.103483

NM_005965	841308	Hs.211582	AL035878	896968	Hs.34780
BC017409	1696831	Hs.88594	AA830549	859192	Hs.20021
BC017409	486626	Hs.88594	AA630788	825470	Hs.156346
AW139590	1571882	Hs.156051	AI831078	1620905	Hs.14587
NM_006235	1541958	Hs.2407	NM_001337	283023	Hs.78913
AB037715	32122	Hs.183639	AB032417	1891563	Hs.19545
AI424409	1493107	Hs.348909	AK027146	469235	Hs.180946
AF002672	2502722	Hs.152944	AW293219	785694	Hs.288467
BC008651	50892	Hs.23133	BF513346	841480	Hs.88780
M87507	120106	Hs.2490	BC009198	746373	Hs.348989
BF508058	744374	Hs.4996	BC014890	293339	Hs.93005
AI888490	666707	Hs.55902	AF339783	72811	Hs.288809
AF104313	782460	Hs.173374	AB017800	781091	Hs.6414
BF056618	2019526	Hs.233634	AI434326	1435103	Hs.5541
AL136842	683059	Hs.260024	BC001638	774082	Hs.1619
M85294	323185	Hs.274382	AI733703	1742850	Hs.143735
BC017703	884789	Hs.57672	AF141332	3117993	Hs.200333
BC014117	143443	Hs.2001	NM_003221	363144	Hs.33102
U60975	2413337	Hs.278571	AL137559	767475	Hs.27495
AF105378	1569187	Hs.8040	AF131794	843250	Hs.10432
AL137662	85193	Hs.274401	AF131794	950450	Hs.10432
AL134596	2098508	Hs.89512	AF101477	2345693	Hs.144914
BC015496	180803	Hs.32309	AL046192	2165360	Hs.8854
AW291368	196435	Hs.34455	AL046192	295410	Hs.8854
AK027121	795746	Hs.38178	AL046192	563985	Hs.8854
AF062595	39600	Hs.18268	U43203	81427	Hs.197764
AK025796	595420	Hs.239218	AI096369	668007	Hs.348862
BC005359	2016194	Hs.151413	AL136703	854678	Hs.57209
AA731869	1847618	Hs.1309	AF033347	45636	Hs.40866
BC016757	502142	Hs.20985	AI260476	786605	Hs.71992
BM141806	772373	Hs.47094	AI559983	712505	Hs.334562
BC002415	823928	Hs.1581	BE551149	1620366	Hs.129319
NM_057749	773345	Hs.30464	AI373912	611407	Hs.241363
M26683	768561	Hs.303649	AI823489	1609665	Hs.167218
BC010690	1554167	Hs.334703	AW131780	1883065	Hs.167988
NM_000795	2017689	Hs.73893	AW131780	2164744	Hs.167988
BC005055	1049346	Hs.274344	AA912183	284383	Hs.47447
N93663	307019	Hs.118240	L20971	788136	Hs.188
AI311898	2047361	Hs.140197	AK026315	79565	Hs.178470
AI732388	159362	Hs.177576	AK001643	1585650	Hs.8395
AI869243	898249	Hs.17882	AI144219	138917	Hs.92137
AI740671	299274	Hs.351568	BC000897	755599	Hs.146360
BC012113	1592715	Hs.166146	AL110174	2306752	Hs.90005
AF097021	2312470	Hs.273321	R43523	32777	Hs.217754
AB058769	754126	Hs.334838	BM126079	1894405	Hs.124130
AF263462	296444	Hs.18376	BF477905	366209	Hs.58104
AL137686	712166	Hs.182982	AA777592	71116	Hs.288582
R56080	34888	Hs.12246	NM_003512	283919	Hs.28777
NM_005906	1841007	Hs.148496	NM_002538	1881469	Hs.171952
AA603977	2321042	Hs.218366	BC018112	857002	Hs.75969

AI765908	1883327	Hs.129166
AI216751	1884505	Hs.143977
AA767639	34149	Hs.79170
BC002745	789147	Hs.146580
U49395	486678	Hs.77807
AL110131	726599	Hs.28783
BC005305	2322038	Hs.408
AI571426	841282	Hs.105700
AA398015	726645	Hs.287364
AB012643	1475595	Hs.250769
M93119	22895	Hs.89584
AI703322	108330	Hs.103253
AW453001	487820	Hs.76722
AA937401	1569876	Hs.13234
AF059617	795877	Hs.3838
AA910331	491692	Hs.119129
BC002718	1759582	Hs.10086
AJ315514	784296	Hs.1790
AI560576	146123	Hs.79005
BC001645	897822	Hs.74101
BC017073	128695	Hs.22015
AF009227	155716	Hs.172816
AF054181	809455	Hs.183435
AF222340	725126	Hs.247043
BC016719	626348	Hs.17558
AA806859	147651	Hs.266957
AK024697	300632	Hs.25477
AI961887	418262	Hs.119571
AI089428	278404	Hs.21964
AF257182	430717	Hs.160271
AK026256	796079	Hs.289015
BE349538	826256	Hs.15791
AA831508	366830	Hs.32553
AI766890	428163	Hs.30022
NM_005923	1880757	Hs.151988
NM_000609	2239290	Hs.237356
AL137274	742642	Hs.11169
AW084130	1468820	Hs.166373
AK027036	490329	Hs.61345
NM_014583	786550	Hs.279943
BE670572	430237	Hs.181297
W46976	325070	Hs.94667
AI268717	1910959	Hs.128401
NM_001773	213635	Hs.85289
AL353948	343079	Hs.6272
U90914	1896838	Hs.5057
AI733236	1909535	Hs.128312
BC001350	50480	Hs.172851
AK025346	812256	Hs.48965
NM_001873	40558	Hs.75360

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

EXAMPLES

Example I:

Clinical specimen collection and clinicopathological parameters. 86 patients were expression profiled, 57 of these had clinical follow-up, specifically overall survival. Biomarker status is shown below in Table 3 for all 86 patients

Table 3: Age and biomarker status for the 86 patients subsequently gene expression profiled

		No. of Cases	Percentage
Age	<45	12	14%
	45-55	24	28%
	>55	50	58%
Estrogen-receptor status	positive	41	48%
	negative	45	52%
Progesterone-receptor status	positive	32	37%
	negative	54	63%
Her2/Neu status	positive	16	19%
	intermediate	23	27%
	negative	45	54%

The estrogen receptor (ER) status profile was discovered by the following steps

- (i) patient biopsy set was divided up into two groups based on prior knowledge of their respective ER status (ER-positive and ER-negative);
- (ii) a standard t-test was completed on each gene to identify genes whose expression was different between ER-/+; and
- (iii) the P values were adjusted via the Benjamini-Hochberg false discovery rate method procedure for the inclusion of all genes which had $p < 0.05$.

This example was used for a hierarchical clustering of 86 patients with an overall total of 3,105 genes that correspond to an ER signature. The results are shown in Tables 1 and 2.

Example II:

Frozen biological breast cancer samples from 247 patients were used for expression profiling to identify genes that correlate with ER+ and ER- states in a manner analogous to the previous example. The analysis identified 2608 genes that correlated with one of two ER states. The results are shown in Tables 3 and 4.

All references cited herein, including patents, patent applications, and publications, are hereby incorporated by reference in their entireties, whether previously specifically incorporated or not.

Having now fully described this invention, it will be appreciated by those skilled in the art that the same can be performed within a wide range of equivalent parameters, concentrations, and conditions without departing from the spirit and scope of the invention and without undue experimentation.

While this invention has been described in connection with specific embodiments thereof, it will be understood that it is capable of further modifications. This application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure as come within known or customary practice

within the art to which the invention pertains and as may be applied to the essential features hereinbefore set forth.

We claim:

1. An array comprising polynucleotide probes capable of hybridizing to nucleic acid molecules of one or more of the genes listed in Table 1, 2, 3, or 4 and comprising sequences within 350 nucleotides of the polyadenylation site of said genes, said probes hybridized to nucleic acids derived from a cell of a subject afflicted with, or suspected of having, breast cancer .
2. The array of claim 1 comprising 11 or more of the genes in Table 1, 2, 3, or 4.
3. The array of claim 2 comprising all the genes in Table 1, 2, 3, or 4.
4. The array of any one of claims 1-3 wherein said cell is from a human subject or such a subject afflicted with breast cancer.
5. The array of any one of claims 1-4 wherein said nucleic acids derived from one or more breast cancer cells are prepared by mRNA amplification.
6. The array of any one of claims 1-4 wherein said nucleic acids derived from one or more breast cancer cells are cDNA.
7. The array of any one of the preceding claims wherein said cell is in a section of tissue from a subject or is microdissected from said section.
8. A method to determine the ER status of breast cancer cells in a sample from a subject comprising assaying said sample for expression of one or more genes in Table 1 or 3 and/or one or more genes in Table 2 or 4.

9. The method of claim 8 wherein said assaying comprises preparing RNA, optionally labeled, from said sample and optionally converting said RNA into cDNA, optionally labeled.

10. The method of claim 9 wherein said RNA is not labeled and used for quantitative PCR.

11. The method of claim 8 wherein said assaying comprises using an array.

12. The method of any one of claims 8-11 wherein said sample is a ductal lavage or fine needle aspiration or FFPE breast tissue sample.

13. The method of claim 12 wherein said sample is microdissected to isolate one or more cells that are breast cancer cells or suspected of being breast cancer cells.

14. The method of any one of claims 8-13 further comprising determination of the ratio of the expression of a gene in Table 1 or 3 to the expression of a gene in Table 2 or 4 as an indicator of ER status.

15. A method to determine therapeutic treatment for a patient having breast cancer comprising
identifying said patient as being ER positive or ER negative after assaying breast cancer cells of said patient for expression of one or more genes listed in Table 1, 2, 3, and/or 4 and
selecting the appropriate treatment for a patient having cells of such ER status.

16. The method of claim 15 wherein said assaying comprises preparing RNA, optionally labeled, from said sample and optionally converting said RNA into cDNA, optionally labeled.

17. The method of claim 16 wherein said RNA is not labeled and used for quantitative PCR.
18. The method of claim 16 wherein said assaying comprises using an array.
19. The method of any one of claims 15-18 wherein said sample is a ductal lavage or fine needle aspiration or FFPE breast tissue sample.
20. The method of claim 19 wherein said sample is microdissected to isolate one or more cells that are breast cancer cells or suspected of being breast cancer cells.
21. The method of any one of claims 15-20 wherein said assaying comprises determination of the ratio of the expression of a gene in Table 1 or 3 to the expression of a gene in Table 2 or 4 as an indicator of ER status.

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
16 September 2004 (16.09.2004)

PCT

(10) International Publication Number
WO 2004/079014 A3

- (51) International Patent Classification⁷: **C12Q 1/68**,
G01N 33/574
- (21) International Application Number:
PCT/US2004/006736
- (22) International Filing Date: 4 March 2004 (04.03.2004)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
60/451,942 4 March 2003 (04.03.2003) US
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- (81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.
- (84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).
- Published:**
— with international search report
— before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments
- (88) Date of publication of the international search report:
31 March 2005
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: SIGNATURES OF ER STATUS IN BREAST CANCER

(57) Abstract: The invention relates to the identification and use of gene expression profiles, or patterns, suitable for identification of populations that are positive and negative for estrogen receptor expression. The gene expression profiles may be embodied in nucleic acid expression, protein expression, or other expression formats, and may be used in the study and/or diagnosis of cells and tissue in breast cancer as well as for the study and/or determination of prognosis of a patient, including breast cancer survival.



WO 2004/079014 A3

INTERNATIONAL SEARCH REPORT

Application No

PCT/US2004/006736

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12Q1/68 G01N33/574

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the International search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, EMBASE, WPI Data, PAJ

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE GEO NCBI; 11 March 2002 (2002-03-11), "Affymetrix GeneChip Human Genome U95 Set HG-U95A" XP002293987 retrieved from NCBI Database accession no. GPL91 *Invention 1* Pobe ID 35832_at KIAA1077 protein GenBank Accession AB029000 abstract page 113, line 13 ----- -/-	1,4-7

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"Z" document member of the same patent family

Date of the actual completion of the international search

26 August 2004

Date of mailing of the international search report

01.02.05

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INTERNATIONAL SEARCH REPORT

Application No

PCT/US2004/O06736

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 02/059271 A (ORR MICHAEL S ; DIGGANS JAMES C (US); GENE LOGIC INC (US); NATION MICH) 1 August 2002 (2002-08-01) the whole document *Invention 1* page 34, lines 6-8; claims 1,24; table 1	1,4-7
X	WO 02/059377 A (EOS BIOTECHNOLOGY INC) 1 August 2002 (2002-08-01) *Invention 1* the whole document page 142, line 55; claim 1 page 8, lines 9-12	1,4-7
P,X	NAGAI MARIA APARECIDA ET AL: "Differentially expressed genes and estrogen receptor status in breast cancer." INTERNATIONAL JOURNAL OF ONCOLOGY, vol. 23, no. 5, November 2003 (2003-11), pages 1425-1430, XP002293985 ISSN: 1019-6439 *Invnetion 1* the whole document table II	1,4-21
A	WO 02/103320 A (ROSETTA INPHARMATICS INC) 27 December 2002 (2002-12-27) the whole document page 4, lines 5-10; table 1 page 107 - page 116	1,4-21
A	RAJA RAJIV ET AL: "A microgenomics platform for high-throughput gene expression analysis of pure cell populations." JOURNAL OF CLINICAL LIGAND ASSAY, vol. 25, no. 3, October 2002 (2002-10), pages 253-259, XP009035629 ISSN: 1081-1672 the whole document page 258, left-hand column, last paragraph; table 1	1,4-21

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2004/006736

Box II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 1, 3-21 (all partially), 2
because they relate to subject matter not required to be searched by this Authority, namely:
Although claims 15-21 are directed to a diagnostic method practised on the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☒ Claims Nos.: 1, 3-21 (all partially), 2
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1, 4-21 (in part)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box II.1

Although claims 15-21 are directed to a diagnostic method practised on the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

Continuation of Box II.2

Claims Nos.: 1, 3-21 (all partially), 2

Present claims 1, 3-21 (all partially), 2 relate to an extremely large number of possible combination of genes to be used in the claimed arrays and methods due to the expressions "one or more of the genes listed in Tables 1-4" (independent claims 1, 8, 15) and "comprising 11 or more of the genes in Tables 1-4" (claim 2). In fact, the claims contain so many possible permutations that a lack of clarity (and conciseness) within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search of the claims impossible and also renders a listing of different inventions which would belong to a single inventive concept impossible.

(Please consider that claim 2 alone covers
525.009.494.813.685.200.000.000.000.000.000 different arrays).

As in addition the application discloses no particular combination of genes to be used in the arrays and methods, support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT is to be found for none of such particular arrays and/or methods. In the present case, the claims so lack support, and the application so lacks disclosure, that neither a meaningful search even for particular parts of such claims is possible, nor the listing of individual such combinations as separate inventions and asking for additional search fees for such particular combinations is reasonable. Consequently, the search has been carried out for subject-matter relating to the KIAA1077 gene (as listed first in Table 1)(claims 1, 3-21 all partially), whereas subject-matter comprising in addition "more of the genes listed in Tables 1-4" (claims 1, 3-21 all partially) or comprising in addition 10 or more of the genes in Table 1-4 (claim 2) has been excluded from the search.

The applicant's attention is drawn to the fact that claims relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure. If the application proceeds into the regional phase before the EPO, the applicant is reminded that a search may be carried out during examination before the EPO (see EPO Guideline C-VI, 8.5), should the problems which led to the Article 17(2) declaration be

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

overcome.

INTERNATIONAL SEARCH REPORT

Information on patent family members

Application No

PCT/US2004/006736

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
WO 02059271	A	01-08-2002	WO	02059271 A2	01-08-2002
WO 02059377	A	01-08-2002	US	2004146862 A1	29-07-2004
			CA	2440703 A1	01-08-2002
			EP	1425302 A2	09-06-2004
			WO	02059377 A2	01-08-2002
			US	2004029114 A1	12-02-2004
WO 02103320	A	27-12-2002	CA	2451074 A1	27-12-2002
			EP	1410011 A2	21-04-2004
			WO	02103320 A2	27-12-2002
			US	2003224374 A1	04-12-2003
			US	2004058340 A1	25-03-2004

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